



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 116910

TO: Karen A Lacourciere

Location: rem/2d15/2c18

Art Unit: 1635

March 22, 2004

Case Serial Number: 09/260624

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

STIC-Biotech/ChemLib

116910

From: Fredman, Jeffrey
Sent: Wednesday, March 17, 2004 9:53 AM
To: STIC-Biotech/ChemLib
Cc: Lacourciere, Karen
Subject: FW: Rush sequence search approval 09/260,624

RECEIVED
MAR 17 2004
STIC

This was already submitted, but if possible please rush.

I Approve.

Jeff Fredman

-----Original Message-----

From: Lacourciere, Karen
Sent: Monday, March 15, 2004 11:13 AM
To: Fredman, Jeffrey
Subject: Rush sequence search approval 09/260,624

Hi Jeff-

Could you approve a RUSH for this search? The case is about to hit the 4 month date, Jhn wants it done ASAP. The search by the prior Examiner is not in the case and the claims have been broadened that new art will probably need to be applied.

Thank you!
Karen

Please search SEQ ID NO:1 and 2 in the commercial databases and in pre-grant pubs.
Thank-you

Karen A. Lacourciere Ph.D.

Remsen 2D15 GAU 1635
(571) 272-0759
mailbox Remsen 2C18

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 3/22/04
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:50:14 ; Search time 2409 Seconds
(without alignments)
185.941 Million cell updates/sec

Title: US-09-260-624A-2
Perfect score: 15
Sequence: 1 cgtatgacagatctg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estlin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estcom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pin:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_pig:*
 - 27: em_gss_vxl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	100.0	220	13	BQ226183
C 2	15	100.0	226	10	BG001759
C 3	15	100.0	230	14	T19802
C 4	15	100.0	239	10	BF086893

C 5	15	100.0	246	10	BF085986
C 6	15	100.0	342	29	CG566143
C 7	15	100.0	351	13	BQ316480
C 8	15	100.0	353	13	BQ316481
C 9	15	100.0	413	12	BG797804
C 10	15	100.0	414	12	BM796675
C 11	15	100.0	423	14	CA560591
C 12	15	100.0	423	29	CG641066
C 13	15	100.0	424	29	CG616284
C 14	15	100.0	433	14	N72527
C 15	15	100.0	436	9	AA474058
C 16	15	100.0	436	29	CG583628
C 17	15	100.0	446	29	CG594299
C 18	15	100.0	446	29	CG801951
C 19	15	100.0	453	29	CG591152
C 20	15	100.0	455	29	CG604679
C 21	15	100.0	477	29	CG568851
C 22	15	100.0	480	29	CG597990
C 23	15	100.0	487	14	CF139164
C 24	15	100.0	490	14	CB220639
C 25	15	100.0	511	29	CG836459
C 26	15	100.0	595	13	BG898500
C 27	15	100.0	617	14	CF951196
C 28	15	100.0	619	14	CA531310
C 29	15	100.0	640	10	BB614123
C 30	15	100.0	651	12	BG480368
C 31	15	100.0	651	29	CG533806
C 32	15	100.0	661	10	BE779265
C 33	15	100.0	661	13	BY744039
C 34	15	100.0	667	10	BF468350
C 35	15	100.0	673	12	BM011814
C 36	15	100.0	673	13	BY744015
C 37	15	100.0	677	29	AG131725
C 38	15	100.0	682	10	BB643278
C 39	15	100.0	683	10	BF313295
C 40	15	100.0	688	12	BG325079
C 41	15	100.0	693	13	BY734800
C 42	15	100.0	699	10	BF461108
C 43	15	100.0	701	10	BE312219
C 44	15	100.0	706	10	BF313593
C 45	15	100.0	708	12	BI826961

ALIGNMENTS

RESULT 1
BQ226183/c
LOCUS BQ226183 220 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7572631 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6044738
5', mRNA sequence.
ACCESSION BQ226183
VERSION BQ226183.1 GI:20407583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 220)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL13287 row: n column: 03
High quality sequence start: 25

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

High quality sequence stop: 219.

FEATURES

Location/Qualifiers
1..220
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6044738"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 220;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 44 CGTATGACAGATCTG 30

RESULT 2

BG001759/c
LOCUS
DEFINITION CM3-GN0049-151100-359-f10 GN0049 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG001759
VERSION BG001759.1 GI:12440410
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 226)
AUTHORS Dias Neto, E., Garcia Correa, R., Vertovski-Almeida, S., Briones, M.R., Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Sucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202683
PubMed 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-GN0049-151100-359-f10&t3=2000-11-15&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence stop: 226.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0049"
/note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning

products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 219 CGTATGACAGATCTG 205

RESULT 3

T19802
LOCUS
DEFINITION T19802 B555F Heart Homo sapiens cDNA clone B555 similar to RecA-like protein HeRad51, mRNA sequence.
ACCESSION T19802
VERSION T19802.1 GI:597547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 230)
AUTHORS Liew, C.C., Hwang, D.M., Fung, Y.W., Laurensen, C., Cukerman, E., Tsui, S. and Lee, C.Y.
TITLE A catalogue of genes in the cardiovascular system as identified by expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)
MEDLINE 95024171
PubMed 7938007
COMMENT Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 61779750995
Email: cilew@rics.bwh.harvard.edu
Seq primer: GGTGGCAGCAGCTCTCTGGAGCC.

FEATURES

Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B555"
/lab_host="E.coli Y1090"
/clone_lib="Heart"
/note="Vector: Lambda gt11; Site 1: EcoRI; Site 2: EcoRI"

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 36 CGTATGACAGATCTG 50

RESULT 4

BF086893/c
LOCUS
DEFINITION CM3-GN0092-160900-353-c03 GN0092 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF086893
VERSION BF086893.1 GI:10892603
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 239)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL
 MEDLINE
 PUBLISHED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM3-GN0092-160
 900-353-c03&t3=2000-09-16&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 25
 High quality sequence stop: 239.

FEATURES
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 1..239
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0092"
 /note="Organ: placenta normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 239;
 Best Local Similarity 100.0%; Pred. NO. 7.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
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 DB 232 CGTATGACAGATCTG 218

RESULT 5
 BF085986/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 246)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL
 MEDLINE
 PUBLISHED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM3-GN0092-160
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 Seq primer: puc 18 forward
 High quality sequence start: 25
 High quality sequence stop: 239.

FEATURES
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 /mol_type="mRNA"
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 SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 239;
 Best Local Similarity 100.0%; Pred. NO. 7.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 |||||
 DB 232 CGTATGACAGATCTG 218

RESULT 5
 BF085986/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 246)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 MEDLINE
 PUBLISHED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=CM3-GN0047-160
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 High quality sequence stop: 246.

FEATURES
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 /organism="Homo sapiens"
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 SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
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 Best Local Similarity 100.0%; Pred. NO. 8e+02;
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 QY 1 CGTATGACAGATCTG 15
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 DB 239 CGTATGACAGATCTG 225

RESULT 6
 CG566143/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 342)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slighthorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
 wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

TITLE
 wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL
 MEDLINE
 PUBLISHED
 COMMENT
 Contact: Zambrowicz BP
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as

FEATURES
 source
 1..342
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="cDNA"
 /db_xref="taxon:10116"
 /dev_stage="Embryo"
 /clone_lib="EST"
 /note="Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in the text."

ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 342 bp
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
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RESULT 6
 CG566143/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 342)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggett,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slighthorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
 wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

TITLE
 wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL
 MEDLINE
 PUBLISHED
 COMMENT
 Contact: Zambrowicz BP
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

FEATURES

source

Location/Qualifiers
1..342
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST191539"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 342;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 324 CGTATGACAGATCTG 310

RESULT 7

BQ316480/c
LOCUS BQ316480 351 bp mRNA linear EST 17-MAY-2002
DEFINITION PM4-CT0331-291199-001-A06 CT0331 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ316480
VERSION BQ316480.1 GI:20922249
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 351)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0331-
291199-001-A06&t3=1999-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 351.
Location/Qualifiers
1..351
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0331"
/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low

FEATURES

source
1..351
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0331"
/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 353;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 152 CGTATGACAGATCTG 138

stringency conditions."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

Db 150 CGTATGACAGATCTG 136

RESULT 8

BQ316481/c
LOCUS BQ316481 353 bp mRNA linear EST 17-MAY-2002
DEFINITION PM4-CT0331-291199-001-A11 CT0331 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ316481
VERSION BQ316481.1 GI:20922250
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 353)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-CT0331-
291199-001-A11&t3=1999-11-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 353.
Location/Qualifiers
1..353
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0331"
/notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low

```

RESULT 9
BG797804
LOCUS
DEFINITION ic07a08.x1 Kaestner ngn3 - 413 bp mRNA linear EST 05-JUL-2001
SW:RAB1_RABIT_077507 DNA REPAIR PROTEIN RAD51 HOMOLOG 1. i, mRNA
sequence.
ACCESSION BG797804
VERSION BG797804.1 GI:14144906
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Melton, D., Brown, J., Kent, G., Permutt, A., Lee, C., Kaestner, K.,
Lenishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blustain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, K., Tsagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8857
Email: dmelton@biohp.harvard.edu
Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000) Library was constructed by Catherine Lee DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Marie Scarce
(mscarce@mail.med.upenn.edu)
High quality sequence stop: 367.
FEATURES
source
1..413
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/SV x CD1"
/db_xref="taxon:10090"
/dev_stage="p.c. 14.5"
/clone_lib="Kaestner ngn3 -"
/lab_host="E. coli-DH12S (GIBCO)"
/notes="Organ: pancreas; Vector: pSPORT2 (GIBCO); Site_1:
Not 1; Site_2: Sal I; The library was prepared by
Catherine S. Lee and has not been published. The pancreas
was obtained from Gerard Gradwohl (PNAS 97 P1607-1611,
2000). The cDNA's were prepared with an oligo containing a
NotI site, and SalI linkers were added to the ends. The
inserts were cut with NotI before being cloned into the
NotI-SalI sites in the vectors. This is one of two
libraries, ngn3 wt and ngn3 -/- . The ngn3 -/- library is
in pSPORT2, T7 promoter is 3'."
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 413;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
|||||
Db 187 CGTATGACAGATCTG 201

RESULT 10
BM796675/c
LOCUS
DEFINITION K-EST0079458 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-64-E10
5', mRNA sequence.
ACCESSION BM796675
VERSION BM796675.1 GI:19144907
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 414)
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.B., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 64 row: E column: 10
High quality sequence stop: 414.
FEATURES
source
1..414
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-64-E10"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="SNU-16"
/clone_lib="S22SNU16n1"
/notes="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
ORIGIN
Query Match 100.0%; Score 15; DB 12; Length 414;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
|||||
Db 333 CGTATGACAGATCTG 319

RESULT 11
CA560591/c
LOCUS
DEFINITION K0274F02-5N NIA Mouse Unfertilized Egg cDNA Library (long) Mus
musculus cDNA clone NIA:K0274F02 IMAGE:30051805 5', mRNA sequence.
ACCESSION CA560591
VERSION CA560591.1 GI:25105246
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 423)
AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Staggs, C.A.,
Martin, P., Aiba, K., Tanaka, T. and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(long)
JOURNAL Unpublished (2001)
COMMENT Contact: Dawood B. Dudekula

```

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K027A row: F column: 02
Seq primer: M13 Reverse
High quality sequence stop: 423
POLYA=No.

FEATURES

source

Location/Qualifiers

1. .423
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="NIA:K0274F02 IMAGE:30051805"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI. Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]]. Total RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
5'-pGACTAGTCTGAGTCGGAGCGCGCCCTTTTCTTTT-3'), treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. NO. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

|||||
302 CGTATGACAGATCTG 288

Db

RESULT 12

CG641066/c

LOCUS

CG641066 423 bp DNA linear GSS 02-OCT-2003
OST375200 Mus musculus 129Sv/Ev Mus musculus genomic clone

DEFINITION OST375200, Genomic survey sequence.

ACCESSION CG641066

VERSION CG641066.1 GI:37464915

KEYWORDS GSS.

SOURCE Mus musculus

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 423)
Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J., Piggott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A., Friddle C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C., Key B.W. Jr., Kipp P., Kohlhauff B., Ma Z.-Q., Markesich D., Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z., Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N., Zhu Q., Person C. and Sands A.T.

TITLE

JOURNAL

COMMENT

Zhu, Q., Person, C. and Sands, A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14103-14114 (2003)
Contact: Zambrowicz BP
Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

source

Location/Qualifiers

1. .423
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST375200"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 423;
Best Local Similarity 100.0%; Pred. NO. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15

|||||
416 CGTATGACAGATCTG 402

Db

RESULT 13

CG616284/c

LOCUS

CG616284 424 bp DNA linear GSS 02-OCT-2003
OST308246 Mus musculus 129Sv/Ev Mus musculus genomic clone

DEFINITION OST308246, genomic survey sequence.

ACCESSION CG616284

VERSION CG616284.1 GI:37440133

KEYWORDS GSS.

SOURCE Mus musculus

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 424)
Zambrowicz B.P., Abuin A., Ramirez-Solis R., Richter L.J., Piggott J., BeltrandelRio H., Buxton E.C., Edwards J., Finch R.A., Friddle C.J., Gupta A., Hansen G., Hu Y., Huang W., Jaing C., Key B.W. Jr., Kipp P., Kohlhauff B., Ma Z.-Q., Markesich D., Payne R., Potter D.G., Qian N., Shaw J., Schrick J., Shi Z.-Z., Sparks M.J., Van Sligtenhorst I., Vogel P., Walke W., Xu N., Zhu Q., Person C. and Sands A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14103-14114 (2003)
Contact: Zambrowicz BP
Omnibank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

source

Location/Qualifiers

1. .424
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST308246"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN


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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 417 CGTATGACAGATCTG 403

RESULT 14
N72527/c
LOCUS
DEFINITION
Yv43h12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:245543 5', similar to gb:V00493 rnal HEMOGLOBIN ALPHA CHAIN
(HUMAN); contains element MER22 repetitive element ; , mRNA sequence.
N72527
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
1 (bases 1 to 433)
Hillier,L., Clark,N., Dubuque,T., Eliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,S.E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LInL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 355 Std Error: 0.00
Seq primer: reverse ET
High quality sequence stop: 384.
Location/Qualifiers
1. 433
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3794789"
/db_xref="taxon:9606"
/clone="IMAGE:245543"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5', AACCTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match      100.0%; Score 15; DB 14; Length 433;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 67 CGTATGACAGATCTG 53

Query Match      100.0%; Score 15; DB 29; Length 424;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 417 CGTATGACAGATCTG 403

RESULT 15
AA474058/c
LOCUS
DEFINITION
v554c11.r1 Beddington mouse embryonic region Mus musculus CDNA
clone IMAGE:821972 5', similar to gb:D14134 DNA REPAIR PROTEIN RAD51
HOMOLOG (HUMAN); gb:D13803 Mouse mRNA for RECA-like protein
MmrRad51, complete cds (MOUSE); , mRNA sequence.
AA474058
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
REFERENCE
1 (bases 1 to 436)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
JOURNAL
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LInL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:490252
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 229.
Location/Qualifiers
1. 436
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6 x DBA"
/db_xref="taxon:10090"
/clone="IMAGE:821972"
/sex="pooled"
/tissue_type="embryo"
/dev_stage="7.5dpc"
/lab_host="DH12S"
/clone_lib="Beddington mouse embryonic region"
/note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Gastrulating embryos were collected at 7.5dpc
from C57BL6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
Referenced in Development 121, 2479-2489 (1995)"

ORIGIN
Query Match      100.0%; Score 15; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 243 CGTATGACAGATCTG 229

Search completed: March 21, 2004, 23:22:49
Job time : 2423 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:50:14 ; Search time 2409 Seconds
(without alignments)
185.941 Million cell updates/sec

Title: US-09-260-624A-1

Perfect score: 15

Sequence: 1 ggcttcaataatcc 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	269	AQ463196	AQ463196 HS 5199 B
2	15	100.0	328	BU221983	BU221983 603756554
3	15	100.0	396	CA531739	CA531739 C0324803
4	15	100.0	404	BY227299	BY227299 BY227299

C 5	15	100.0	414	12	BM796675
C 6	15	100.0	423	14	CA560591
C 7	15	100.0	423	29	CG641066
C 8	15	100.0	427	13	EX494877
C 9	15	100.0	436	9	AA474058
C 10	15	100.0	437	12	BG798213
C 11	15	100.0	446	29	CG594299
C 12	15	100.0	446	29	CG601951
C 13	15	100.0	449	13	BY030621
C 14	15	100.0	453	29	CG591152
C 15	15	100.0	454	13	EX475529
C 16	15	100.0	455	29	CG604879
C 17	15	100.0	467	13	BY030677
C 18	15	100.0	471	13	BY030677
C 19	15	100.0	479	14	CA557006
C 20	15	100.0	480	29	CG597990
C 21	15	100.0	511	12	BI067879
C 22	15	100.0	511	29	CG526459
C 23	15	100.0	512	13	BU252761
C 24	15	100.0	533	13	BX260018
C 25	15	100.0	533	14	CD562647
C 26	15	100.0	534	12	BG085688
C 27	15	100.0	534	29	AY418335
C 28	15	100.0	534	29	AY418336
C 29	15	100.0	534	29	AY418337
C 30	15	100.0	537	10	BB858442
C 31	15	100.0	545	14	CD562793
C 32	15	100.0	547	12	BG470554
C 33	15	100.0	548	13	BU202347
C 34	15	100.0	549	10	BE280848
C 35	15	100.0	564	9	AA940166
C 36	15	100.0	584	12	BI193363
C 37	15	100.0	585	13	BU449906
C 38	15	100.0	574	9	AUL23935
C 39	15	100.0	590	14	CF899075
C 40	15	100.0	595	13	BU988500
C 41	15	100.0	615	10	BE913664
C 42	15	100.0	619	14	CA531310
C 43	15	100.0	622	12	BG474115
C 44	15	100.0	625	13	BU135803
C 45	15	100.0	626	13	BU335269

ALIGNMENTS

AQ463196 269 bp DNA linear GSS 23-APR-1999
HS 5199 B1 E10 T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=775 Col=19 Row=J, genomic survey sequence.

ACCESSION AQ463196
VERSION AQ463196.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 269)

MAHAIKAS, G.G., WALLACE, J.C., SMITH, K., SWARTZELL, S., HOLZMAN, T.,

KELLER, A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAO, S., ADAMS, M.D. and

HOOD, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library PPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong@med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (<http://info@resgen.com>). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 775 row: J column: 19
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 269.
 Location/Qualifiers
 1..269
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="plate=775 Col=19 Row=J"
 /sex="male"
 /clone_lib="RPQI-11 Human Male BAC Library"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 15; DB 28; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 QY 1 GGCTTCACCTAATTC 15
 |||||
 Db 173 GGCTTCACCTAATTC 187

RESULT 2

BU221983/c
 LOCUS BU221983 328 bp mRNA linear EST 25-NOV-2002
 DEFINITION 603756594F1 CSEQCHN04 Gallus gallus cdna clone ChEST668k24 5', mRNA sequence.
 ACCESSION BU221983
 VERSION BU221983.1 GI:25410698
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 1 (bases 1 to 328)
 Boardman, P.E., Sanz-Bzquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 22335534
 MEDLINE 12445392
 CONTACT: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Rubbardeumist.ac.uk.
 Location/Qualifiers
 1..328
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, HiseX"
 /db_xref="taxon:9031"
 /clone="ChEST668k24"
 /tissue_type="whole embryo"
 /dev_stage="20-21"
 /lab_host="DH103"

FEATURES

source

/clone_lib="CSEQCHN04"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; this normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;
 QY 1 GGCTTCACCTAATTC 15
 |||||
 Db 64 GGCTTCACCTAATTC 50

RESULT 3

CAS31739/c
 LOCUS CAS31739 396 bp mRNA linear EST 18-NOV-2002
 DEFINITION C0324B03-SN NIA Mouse Undifferentiated ES Cell cDNA Library (Long) Mus musculus cdna clone NIA:C0324B03 IMAGE:30007118 5', mRNA sequence.
 ACCESSION CAS31739
 VERSION CAS31739.1 GI:25061103
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Luo, A., Jaradat, S.A., Boheler, K.R. and Ko, M.S.H.
 Systematic Analyses of NIA Mouse Undifferentiated ES Cell cDNA Library (Long)
 Unpublished (2001)
 Other_ESRs: C0324B03-3
 Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: C0324 row: B column: 03
 Seq primer: M13 Reverse
 High quality sequence stop: 396
 POLYA=No.

FEATURES

source

Location/Qualifiers
 1..396
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv x 129/Sv-CP"
 /db_xref="niaEST:C0324B03-5N"
 /db_xref="taxon:10090"
 /clone="NIA:C0324B03 IMAGE:30007118"
 /tissue_type="Undifferentiated ES Cell"
 /cell_line="R1 ES cells"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Undifferentiated ES Cell cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were obtained from Dr. Kenneth R. Boheler (National Institute on Aging, USA). ES cells were cultured without feeder cells in the presence of LIF and BRL-conditioned media. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
 5'-pGACTAGTCTGATGCGAGCGCGCCCTTTT-TTTT-3' from 14.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loxe-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The pHI08 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 396;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACATAATCC 15
 |||||
 Db 246 GGCTTCACATAATCC 232

RESULT 4

BY227299/c

LOCUS BY227299 RIKEN full-length enriched, erythroblast Mus musculus cDNA
 clone KOC0009D13 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 404)

REFERENCE

AUTHORS

Okazaki, Y., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schombach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Perlea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S.,
 Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs

TITLE

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Inotani, K., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of genome exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Tissues were provided by Hiromitsu Nakauchi (Dept. of Immunology
 Institute of Basic Medical Sciences University of Tsukuba 1-1-1
 Tennodai, Tsukuba, Ibaraki 305-8578) whose assistance we gratefully
 acknowledge. Please visit our web site
 (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

1..404
 /location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="KOC0009D13"
 /cell_type="erythroblast"
 /clone_lib="RIKEN full-length enriched, erythroblast"

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 404;
 Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACATAATCC 15

|||||

Db 390 GGCTTCACATAATCC 376

RESULT 5

BY227299/c

LOCUS BM796675/414 bp mRNA linear EST 05-MAR-2002
 K-EST0079458 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-64-B10
 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 414)
 Kim, N. S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 64 row: E column: 10
 High quality sequence stop: 414.

FEATURES

source

1. 414
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="S22SNU16n1-64-E10"
 /sex="F"
 /tissue_type="Ascites"
 /cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="DH10B"
 /clone_lib="S22SNU16n1"
 /note="Organ: Stomach; Vector: pRT3-Pac; Site_1: EcoRI; Site_2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 Cell was established from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTCACTAATTC 15
 |||||
 Db 123 GGCCTCACTAATTC 109

RESULT 6

CA560591/c
 LOCUS
 DEFINITION K0274F02-SN NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone NIA:K0274F02 IMAGE:30051805 5', mRNA sequence.
 ACCESSION CA560591
 VERSION CA560591.1 GI:25105246
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 423)
 AUTHORS Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Stagg, C.A., Martin, P., Alha, K., Tanaka, T. and Ko, M.S.H.
 TITLE Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library (long)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0274 row: F column: 02
 Seq primer: M13 Reverse
 High quality sequence stop: 423
 POLYA=No.

FEATURES

Location/Qualifiers

source

1. 423
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="NIA:K0274F02 IMAGE:30051805"
 /tissue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript-enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11541991]. Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen).
 5'-pgactagttctagatcgagcgccgcttttttttttt-3', treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-SalI, purified by phenol/chloroform, and cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Fiao (NIA)."

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 423;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCTCACTAATTC 15
 |||||
 Db 92 GGCCTCACTAATTC 78

RESULT 7

CG641066/c
 LOCUS
 DEFINITION OGT375200 Mus musculus 129Sv/Ev Mus musculus genomic clone OGT375200, genomic survey sequence.
 ACCESSION CG641066
 VERSION CG641066.1 GI:37464915
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 423)
 AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Figgott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fiddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, N.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.
 TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 COMMENT Contact: Zambrowicz BP
 OmilBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

FEATURES

Location/Qualifiers
1..423
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Ev"
/db_xref="taxon:10090"
/clone="OST375200"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATCC 15
|||||
DB 206 GGCTTCACCTAATCC 192

RESULT 8

BX494877/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: MIPS

INGOLSTAEDTER LANDSTR.1, D-85764 NEUHERBERG, GERMANY

THIS IS THE 5' SEQUENCE OF THE CLONE INSERT

CLONE FROM S. WIEMANN, MOLECULAR GENOME ANALYSIS, GERMAN CANCER

RESEARCH CENTER (DKFZ); EMAIL S.WIEMANN@DKFZ-HEIDELBERG.DE;

SEQUENCED BY AGOWA (BERLIN/GERMANY) WITHIN THE CDNA SEQUENCING

CONSORTIUM OF THE GERMAN GENOME PROJECT.

NO SL SEQUENCE AVAILABLE.

THIS CLONE (DKFZP779C0716) IS AVAILABLE AT THE RZPD IN BERLIN.

PLEASE CONTACT THE RZPD: RESSOURCENZENTRUM, HEUBNERWEG 6, 14059

BERLIN-CHARLOTTENBURG, GERMANY; EMAIL: CLONE@RZPD.DE.

Location/Qualifiers

1..427

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZP779C0716"

/tissue_type="liver"

/dev_stage="fetal"

/lab_host="DH10B"

/clone_lib="779 (synonym: hmccl)"

/notes="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 427;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATCC 15
|||||
DB 233 GGCTTCACCTAATCC 219

RESULT 9

AA474058/c

LOCUS

DEFINITION

ve54c11.r1 Beddington mouse embryonic region Mus musculus CDNA

clone IMAGE:821972.5, similar to gb:D141134 DNA REPAIR PROTEIN RAD51

HOMOLOG (HUMAN); gb:D13803 Mouse mRNA for RecA-like protein

Mmrads1, complete cds (MOUSE);, mRNA sequence.

AA474058

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

WashU-HMI Mouse EST Project

Contact: Maxra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 229.

Location/Qualifiers

1..436

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6 x DBA"

/db_xref="taxon:10090"

/clone="IMAGE:821972"

/sex="pooled"

/tissue_type="embryo"

/dev_stage="7.5dpc"

/lab_host="DH128"

/clone_lib="Beddington mouse embryonic region"

/notes="Organ: whole embryo; Vector: pCMV-SPORT; Site 1:

Sall; Site 2: NotI; Cloned unidirectionally. Primer:

Oligo dt. Gastrulating embryos were collected at 7.5dpc

from C57BL6 x DBA matings, excluding embryos that had

developed head folds and all extraembryonic tissues.

Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).

Referenced in Development 121, 2479-2489 (1995)"

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 436;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATCC 15
|||||

DB 33 GGCTTCACCTAATCC 19
|||||

RESULT 10

BG798213/c

LOCUS

DEFINITION

ic07a08.yl Kaestner ngn3 - Mus musculus cdna 5', similar to

SW:RAS1_RABIT 077507 DNA REPAIR PROTEIN RAD51 HOMOLOG 1.; mRNA

sequence.

ACCESSION

VERSION

BG798213

GI:14162545

437 bp mRNA linear EST 05-JUL-2001

ic07a08.yl Kaestner ngn3 - Mus musculus cdna 5', similar to

SW:RAS1_RABIT 077507 DNA REPAIR PROTEIN RAD51 HOMOLOG 1.; mRNA

sequence.

ACCESSION

VERSION

BG798213

GI:14162545

REFERENCE

Zambrowski, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
1 (bases 1 to 446)
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/EV"

AUTHORS

4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES

Source
Location/Qualifiers
1..453
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/EV"
/db_xref="taxon:10090"
/clone="OST245409"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 100.0%; Score 15; DB 29; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

Db 222 GGCTTCACTAATTC 208

RESULT 15

BX475529/c

LOCUS

DEFINITION BX475529 454 bp mRNA linear EST 04-SEP-2003
DKFZp686D04178 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

ACCESSION

BX475529

VERSION

BX475529.1 GI:31672810

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 454)

Baht, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Oeanger, A.,

Fobo, G., Han, M. and Wiemann, S.

EST (Baht, A., Lauber, J., Mewes, H.W., Weil, B., et al.)

Unpublished (2003)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Olgan (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686D04178) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686D04178"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlcc3)"

/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;

cDNA-collection"

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

Db 222 GGCTTCACTAATTC 208

Db 444 GGCTTCACTAATTC 430

Search completed: March 21, 2004, 23:22:35
Job time : 2424 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 20:52:14 ; Search time 53.5 Seconds
(without alignments)
155.594 Million cell updates/sec

Title: US-09-260-624A-2
Sequence: 1 cgtatgcacagatctg 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-454-495-3
2	15	100.0	2229	4	US-09-454-495-1
3	13.4	89.3	213	4	US-09-328-352-2112
4	13.4	89.3	1284	4	US-09-328-352-2004
5	13.4	89.3	1554	1	US-08-463-115-3
6	13.4	89.3	1554	1	US-08-465-388-3
7	13.4	89.3	41171	4	US-08-311-731A-122
8	13.4	89.3	116592	4	US-09-818-512-3
9	13	86.7	1170	4	US-09-491-577-49
10	13	86.7	2787	4	US-09-328-352-977
11	13	86.7	161652	4	US-09-497-855A-40
12	12.4	82.7	30	2	US-08-790-963-35
13	12.4	82.7	30	3	US-09-371-774-35
14	12.4	82.7	261	4	US-09-313-294A-2283
15	12.4	82.7	261	4	US-09-313-294A-2291
16	12.4	82.7	263	4	US-09-976-594-132
17	12.4	82.7	285	4	US-09-313-294A-3505
18	12.4	82.7	480	4	US-09-621-976-13863
19	12.4	82.7	493	4	US-09-621-976-2143
20	12.4	82.7	522	4	US-09-543-681A-1868
21	12.4	82.7	631	4	US-09-833-381-1443
22	12.4	82.7	819	4	US-09-543-681A-1839
23	12.4	82.7	1062	3	US-09-267-031-3
24	12.4	82.7	1167	4	US-09-134-001C-2365
25	12.4	82.7	1224	4	US-09-489-039A-6179
26	12.4	82.7	1276	4	US-09-023-655-705
27	12.4	82.7	2247	4	US-09-710-099-15

28	12.4	82.7	2436	4	US-08-983-275-1	Sequence 1, Appli
29	12.4	82.7	2760	2	US-08-788-674-6	Sequence 6, Appli
30	12.4	82.7	2830	4	US-09-221-017B-730	Sequence 730, App
31	12.4	82.7	3025	4	US-08-961-527-168	Sequence 168, App
32	12.4	82.7	3060	4	US-09-543-681A-275	Sequence 275, App
33	12.4	82.7	3486	4	US-09-543-681A-2314	Sequence 2314, Ap
34	12.4	82.7	4757	1	US-07-865-662F-12	Sequence 12, Appl
35	12.4	82.7	4757	3	US-08-374-219B-12	Sequence 12, Appl
36	12.4	82.7	8351	1	US-08-198-446B-14	Sequence 14, Appl
37	12.4	82.7	8351	2	US-08-870-693-14	Sequence 14, Appl
38	12.4	82.7	9511	1	US-07-925-695-6	Sequence 6, Appli
39	12.4	82.7	9511	1	US-07-925-695-7	Sequence 7, Appli
40	12.4	82.7	36470	4	US-08-311-731A-123	Sequence 123, App
41	12.4	82.7	4403765	3	US-09-103-840A-1	Sequence 2, Appli
42	12.4	82.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
43	12	80.0	161	4	US-09-621-976-19202	Sequence 19202, A
44	12	80.0	277	4	US-09-313-294A-842	Sequence 842, App
45	12	80.0	378	4	US-09-288-143-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-454-495-3
; Sequence 3, Application US/09454495
; Patent No. 6576759
; GENERAL INFORMATION:
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zeng, Hong
; APPLICANT: Vallerga, Anne
; TITLE OF INVENTION: NOVEL ANTISENSE INHIBITION OF RAD51
; FILE REFERENCE: A-67649-1/RMS/DAV/JJD
; CURRENT APPLICATION NUMBER: US/09/454,495
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/119,578
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic.
US-09-454-495-3

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTATGCACAGATCTG 15
| | | | | | | | | | | | | | |
Db 1 CGTATGCACAGATCTG 15

RESULT 2
US-09-454-495-1/c
; Sequence 1, Application US/09454495
; Patent No. 6576759
; GENERAL INFORMATION:
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Zeng, Hong
; APPLICANT: Vallerga, Anne
; APPLICANT: Zarlino, David A.
; TITLE OF INVENTION: NOVEL ANTISENSE INHIBITION OF RAD51
; FILE REFERENCE: A-67649-1/RMS/DAV/JJD
; CURRENT APPLICATION NUMBER: US/09/454,495
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/119,578
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-454-495-1

Query Match 100.0%; Score 15; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||
DB 1758 CGTATGACAGATCTG 1744

RESULT 3

US-09-328-352-2112
; Sequence 2112, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2112
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2112

Query Match 89.3%; Score 13.4; DB 4; Length 213;
Best Local Similarity 93.3%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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DB 103 CGTATGAAGATCTG 117

RESULT 4

US-09-328-352-2004/c
; Sequence 2004, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2004
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2004

Query Match 89.3%; Score 13.4; DB 4; Length 1284;
Best Local Similarity 93.3%; Pred. No. 93;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||
DB 31 CGTATGAAGATCTG 17

RESULT 5

US-08-463-115-3/c
; Sequence 3, Application US/08463115

; Patent No. 5703221
; GENERAL INFORMATION:
; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,115
; FILING DATE: June 5, 1995

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/157,811
; FILING DATE: No. 5703221, December 23, 1993
; APPLICATION NUMBER: 07/887,502
; FILING DATE: May 22, 1992
; APPLICATION NUMBER: 07/704,814
; FILING DATE: May 23, 1991
; APPLICATION NUMBER: 07/763,039
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 213/301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

Four

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-115-3

Query Match 89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
|||
DB 987 CGTATGACCGATCTG 973

RESULT 6

US-08-465-368-3/c
; Sequence 3, Application US/08465388
; Patent No. 5753488
; GENERAL INFORMATION:

; APPLICANT: WILLIAM JOHN MARTIN
; TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
; TITLE OF INVENTION: AND RELATED VACCINES
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-388-3
Query Match 89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGTATGACGATCTG 15
Db 987 CGTATGCCGATCTG 973
RESULT 7
US-08-311-731A-122
Sequence 122, Application US/08311731A
Patent No. 6583286
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-388-3
Query Match 89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGTATGACGATCTG 15
Db 987 CGTATGCCGATCTG 973
RESULT 7
US-08-311-731A-122
Sequence 122, Application US/08311731A
Patent No. 6583286
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-388-3
Query Match 89.3%; Score 13.4; DB 1; Length 1554;
Best Local Similarity 93.3%; Pred. No. 95;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGTATGACGATCTG 15
Db 987 CGTATGCCGATCTG 973
RESULT 7
US-08-311-731A-122
Sequence 122, Application US/08311731A
Patent No. 6583286
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

; APPLICANT: Kim, Hunhyong
; APPLICANT: Clyne, Peter J.
; APPLICANT: Warr, Coral G.
; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
; FILE REFERENCE: 44574-5061-US
; CURRENT APPLICATION NUMBER: US/09/491,577
; CURRENT FILING DATE: 2000-01-25
; EARLIER APPLICATION NUMBER: US 60/117,132
; EARLIER FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1170)
; OTHER INFORMATION: DOR 85A.1
US-09-491-577-49

Query Match 86.7%; Score 13; DB 4; Length 1170;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TATGACAGATCTG 15
|||||
DB 1107 TATGACAGATCTG 1119

RESULT 10
US-09-328-352-977
; Sequence 977, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 977
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-977

Query Match 86.7%; Score 13; DB 4; Length 2787;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATC 13
|||||
DB 2107 CGTATGACAGATC 2119

RESULT 11
US-09-497-855A-40/c
; Sequence 40, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UM01523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 40
; LENGTH: 161652
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-40

Query Match 86.7%; Score 13; DB 4; Length 161652;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TATGACAGATCTG 15
|||||
DB 144144 TATGACAGATCTG 144132

RESULT 12
US-08-790-963-35/c
; Sequence 35, Application US/08790963
; Patent No. 5837464
; GENERAL INFORMATION:
; APPLICANT: Daniel J. Capon
; APPLICANT: Christos John Petropoulos
; TITLE OF INVENTION: Compositions And Methods For
; TITLE OF INVENTION: Determining Anti-viral Drug Susceptibility And
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,963
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 50130-B/JPW/AKC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-790-963-35

Query Match 82.7%; Score 12.4; DB 2; Length 30;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTATGACAGATCTG 15
|||||
DB 19 GTATGACAGATCTG 6

RESULT 13
US-09-371-774-35/c
; Sequence 35, Application US/09371774
; Patent No. 6242187
; GENERAL INFORMATION:
; APPLICANT: Daniel J. Capon

Christos John Petropoulos
 TITLE OF INVENTION: Compositions And Methods For
 Determining Anti-viral Drug Susceptibility And
 Resistance And Anti-viral Drug Screening
 NUMBER OF SEQUENCES: 105
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: United States
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version#1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/371,774
 FILING DATE: 10-Aug-1999
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 50130-F/JPW/CMR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 US-09-371-774-35

Query Match 82.7%; Score 12.4; DB 3; Length 30;
 Best Local Similarity 92.9%; Pred. No. 2.3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTATGACAGATCTG 15
 Db 19 GTATGACAGATCTG 6

RESULT 14
 US-09-313-294A-2283/C
 ; Sequence 2283, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2283
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700552426H1
 US-09-313-294A-2283

Query Match 82.7%; Score 12.4; DB 4; Length 261;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCT 14
 Db 71 CGTATGACAGATCT 58
 RESULT 15
 US-09-313-294A-2291/C
 ; Sequence 2291, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalgudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2291
 ; LENGTH: 261
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700552437H1
 US-09-313-294A-2291
 Query Match 82.7%; Score 12.4; DB 4; Length 261;
 Best Local Similarity 92.9%; Pred. No. 3e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: March 21, 2004, 23:24:42
 Job time : 65.5 secs

Qy 1 CGTATGACAGATCT 14
 Db 71 CGTATGACAGATCT 58

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 18:17:32 ; Search time 282 Seconds
(without alignments)
225.968 Million cell updates/sec

Title: US-09-260-624A-2

Perfect score: 15

Sequence: 1 cgtatgacagatctg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*

- 1: Geneseqn1980a:*
- 2: Geneseqn1980a:*
- 3: Geneseqn2000a:*
- 4: Geneseqn2000a:*
- 5: Geneseqn2000a:*
- 6: Geneseqn2000a:*
- 7: Geneseqn2000a:*
- 8: Geneseqn2000a:*
- 9: Geneseqn2000a:*
- 10: Geneseqn2000a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	3	AAA37713 Human Rad
2	15	100.0	15	4	AAS01195 Human RAD
3	15	100.0	15	4	AAS01204 Human RAD
4	15	100.0	15	6	AA43241 Antisense
5	15	100.0	1024	7	AB283420 Toxicolog
6	15	100.0	1408	2	AAQ91761 Mouse Rad
7	15	100.0	1682	2	AAQ91763 Human Rad
8	15	100.0	1755	2	AAQ64088 Mouse Gen
9	15	100.0	2229	3	AAA37710 Human Rad
10	15	100.0	2229	4	AAS01209 Human RAD
11	14	93.3	470	7	AB223355 Nucleotid
12	14	93.3	510	4	AAH28846 Drosophil
13	14	93.3	513	4	AAH29139 Drosophil
14	14	93.3	649	3	AAFI4202 Aspergill
15	14	93.3	1017	6	ABK72962 Bacillus
16	14	93.3	2684	4	ABL25830 Drosophil
17	14	93.3	3630	4	ABL20510 Drosophil
18	14	93.3	3804	4	ABL20512 Drosophil
19	14	93.3	4053	4	ABL20514 Drosophil
20	14	93.3	5870	4	ABL20514 Drosophil
21	14	93.3	6128	4	ABL20514 Drosophil
22	13.4	89.3	45	6	ABA98655 T-vector-
23	13.4	89.3	183	6	ABA98646 Fragment

24	13.4	89.3	198	6	ABA98660 Fragment
25	13.4	89.3	213	8	ADA30825 DNA encod
26	13.4	89.3	251	3	AAC21220 Human sec
27	13.4	89.3	373	4	AAS5056 Human imm
28	13.4	89.3	398	3	AAH30637 Human col
29	13.4	89.3	410	7	ABX54935 Bovine ES
30	13.4	89.3	783	4	AAH03869 Human cDN
31	13.4	89.3	1284	8	ADA30717 DNA encod
32	13.4	89.3	1554	2	AAV11950 Cytonegal
33	13.4	89.3	1554	2	AAV10137 CMV nucle
34	13.4	89.3	2002	4	AAH45403 Human cDN
35	13.4	89.3	2003	6	ABK87929 Human cer
36	13.4	89.3	2118	4	AAF30809 Human cer
37	13.4	89.3	2118	6	ABK90633 DNA encod
38	13.4	89.3	4649	9	ADB69161 C. neofo
39	13.4	89.3	5266	6	ABA93703 Human sig
40	13.4	89.3	5920	9	ADD48199 Human gen
41	13.4	89.3	8173	4	AAK64969 Human imm
42	13.4	89.3	8173	4	AAS28231 Genomic s
43	13.4	89.3	8350	7	ADA05805 Human NOV
44	13.4	89.3	8350	7	ADA05799 Human NOV
45	13.4	89.3	8487	6	AB233756 Human TRI

ALIGNMENTS

RESULT 1

AAA37713

ID AAA37713 standard; DNA; 15 BP.

AC AAA37713;

XX 22-NOV-2000 (first entry)

XX Human Rad51 antisense inhibitor AS2.

XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;

XX radiation sensitivity; therapy; AS2; ss.

XX Homo sapiens.

XX WO200047231-A2.

XX 17-AUG-2000.

XX 03-FEB-2000; 2000WO-US002881.

XX 10-FEB-1999; 99US-0119578P.

XX 06-DEC-1999; 99US-00454495.

XX (PANG-) PANGENE CORP.

XX Reddy G;

XX WPI; 2000-506091/45.

XX Inhibiting cell proliferation useful for cancer therapy, comprises administering Rad51 inhibitor in vivo.

XX Example 1; Page 25; 42pp; English.

This sequence represents an antisense inhibitor of human Rad51, designated AS2 (also referred to as RS1AS2). The antisense inhibitors can be used in a method of the invention, for inhibiting cell proliferation. They can also be used in methods for inducing sensitivity to radiation and DNA damaging chemotherapeutics in an individual and in a method for prolonging survival in an individual with cancer. The methods and antisense molecules are useful for inhibiting cell proliferation, especially cancerous cell proliferation, for inducing sensitivity to radiation and DNA damaging chemotherapeutics in individuals and for prolonging survival in an individual with cancer. Kits for carrying out the methods may be used to diagnose and/or treat cancer and for

```

CC adjunctive therapy
XX
SQ Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 1 CGTATGACAGATCTG 15

RESULT 2
AAS01195
ID AAS01195 standard; cDNA; 15 BP.
XX
AC AAS01195;
XX
DT 04-JUL-2001 (first entry)
XX
XX Human RAD51 antisense oligonucleotide, AS2.
XX
DE Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
KW arthritis; graft rejection; inflammatory bowel disease; surgery;
KW angioplasty; ss.
XX
OS Homo sapiens.
XX
FN WO200119397-A1.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-US025838.
XX
PR 17-SEP-1999; 99US-0154616P.
PR 06-DEC-1999; 99US-00455300.
XX
XX (PANG-) PANGENE CORP.
XX
PI Reddy G;
XX
PI WPI; 2001-244704/25.
XX
DR Inhibiting cell proliferation for treating arthritis, graft rejection,
PT inflammatory bowel disease, cancer, proliferation induced after medical
PT procedure, involves administering Rad51 antibody or its fragment to cell.
XX
XX Example 6; Fig 16A; 102pp; English.
XX
XX The sequence represents the human Rad51 antisense oligonucleotide, AS2.
CC The antisense oligonucleotide is used to study down-regulation of Rad51
CC protein in human brain, breast and prostate cells. Rad51 protein is
CC defective in repair of damaged DNA, genetic recombination and the
CC recombinational repair of DNA lesions, and plays a central role in
CC cancer. Inhibiting cell proliferation involves administering to a cell a
CC Rad51 antibody or its fragment. The Rad51 antibody or its fragment is
CC useful for inhibiting cell proliferation, for treating disease states
CC such as cancer, autoimmune disease, arthritis, graft rejection,
CC inflammatory bowel disease, proliferation induced after medical
CC procedures such as surgery, angioplasty etc. in humans and animals
XX
XX Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 1 CGTATGACAGATCTG 15

RESULT 3
AAS01204/c
ID AAS01204 standard; cDNA; 15 BP.
XX
AC AAS01204;
XX
DT 04-JUL-2001 (first entry)
XX
XX Human RAD51 sense oligonucleotide, S2.
XX
DE Human; Rad51; drug screening; cancer; autoimmune disease; arthritis;
KW graft rejection; inflammatory bowel disease; surgery; angioplasty; ss.
XX
OS Homo sapiens.
XX
FN WO200119397-A1.
XX
PD 22-MAR-2001.
XX
PF 18-SEP-2000; 2000WO-US025838.
XX
PR 17-SEP-1999; 99US-0154616P.
PR 06-DEC-1999; 99US-00455300.
XX
XX (PANG-) PANGENE CORP.
XX
PI Reddy G;
XX
PI WPI; 2001-244704/25.
XX
DR Inhibiting cell proliferation for treating arthritis, graft rejection,
PT inflammatory bowel disease, cancer, proliferation induced after medical
PT procedure, involves administering Rad51 antibody or its fragment to cell.
XX
XX Example 6; Fig 16D; 102pp; English.
XX
XX The sequence represents the human Rad51 sense oligonucleotide, S2. The
CC sense oligonucleotide is used to study down-regulation of Rad51 protein
CC in human brain, breast and prostate cells. Rad51 protein is defective in
CC repair of damaged DNA, genetic recombination and the recombinational
CC repair of DNA lesions, and plays a central role in cancer. Inhibiting
CC cell proliferation involves administering to a cell a Rad51 antibody or
CC its fragment. The Rad51 antibody or its fragment is useful for inhibiting
CC cell proliferation, for treating disease states such as cancer,
CC autoimmune disease, arthritis, graft rejection, inflammatory bowel
CC disease, proliferation induced after medical procedures such as surgery,
CC angioplasty etc. in humans and animals
XX
XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
Db 1 CGTATGACAGATCTG 15

RESULT 4
AAB43241
ID AAB43241 standard; DNA; 15 BP.
XX
AC AAB43241;
XX
DT 14-NOV-2002 (first entry)
XX
XX Antisense oligonucleotide R51AS2.
XX
DE Tumour cell proliferation; Rad51 inhibitor; p53 protein; premature aging;
KW hyperproliferative disorder; Hodgkin's disease; squamous cell carcinoma;
KW leukaemia; autoimmune disease; cancer; graft rejection; angioplasty;
KW inflammatory bowel disease; immunosuppressive; gene therapy; arthritis;

```


PN JP07143890-A.
XX
PD 06-JUN-1995.
XX
PF 28-MAY-1993; 93JP-00127594.
XX
PR 28-MAY-1993; 93JP-00127594.
XX
PS (TOYM) TOYOBO KK.
PA WPI; 1995-236467/31.
XX P-PSDB; AAR78181.
DR
XX
PT Structural gene encoding RAD51, used in production of RAD51 - used to
PT study drugs against diseases caused by DNA damage, e.g. by UV or X
PT radiation, and to improve efficiency if gene therapy targeting.
XX
PS Claim 1; Page 9-10; 19pp; Japanese.
XX
CC The present sequence, isolated from mouse cDNA and localised to the P1
CC region of chromosome 2, is a specific example of DNA coding for a RAD51
CC protein having the amino acid sequence in AAR78181. The RAD51 protein,
CC which contains an ATP-binding domain, is involved in DNA repair of
CC mismatched base pairs and site-specific recombination in antibody gene
CC rearrangements. The protein binds to double-stranded DNA to form a right-
CC handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-
CC form DNA. As a result, the helix is unwound. The Rad51 gene and the
CC protein it encodes will be useful in designing drugs to treat diseases
CC associated with environmental DNA damage
XX
SQ Sequence 1408 BP; 378 A; 318 C; 392 G; 320 T; 0 U; 0 Other;
Query Match 100.0%; Score 15; DB 2; Length 1408;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTATGACAGATCTG 15
DB 605 CGTATGACAGATCTG 591
RESULT 7
AAQ91763/c
ID AAQ91763 standard; cDNA to mRNA; 1682 BP.
XX
AC AAQ91763;
XX
DT 15-FEB-1996 (first entry)
XX
DE Human Rad51 gene, encodes protein involved in DNA repair.
XX
KW DNA mismatch repair; DNA recombination; site-specific; unwinding;
KW right-handed helical nucleoprotein; RAD51; human; recA; topoisomerase;
KW ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 215..1234
FT /*tag= a
FT /product= "RAD51"
XX
PN JP07143890-A.
XX
PD 06-JUN-1995.
XX
PF 28-MAY-1993; 93JP-00127594.
XX
PR 28-MAY-1993; 93JP-00127594.
XX
PS (TOYM) TOYOBO KK.
PA WPI; 1995-236467/31.
XX
DR
XX
PT Structural gene encoding RAD51, used in production of RAD51 - used to
PT study drugs against diseases caused by DNA damage, e.g. by UV or X
PT radiation, and to improve efficiency if gene therapy targeting.
XX
PS Claim 1; Page 9-10; 19pp; Japanese.
XX
CC The present sequence, isolated from mouse cDNA and localised to the P1
CC region of chromosome 2, is a specific example of DNA coding for a RAD51
CC protein having the amino acid sequence in AAR78181. The RAD51 protein,
CC which contains an ATP-binding domain, is involved in DNA repair of
CC mismatched base pairs and site-specific recombination in antibody gene
CC rearrangements. The protein binds to double-stranded DNA to form a right-
CC handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-
CC form DNA. As a result, the helix is unwound. The Rad51 gene and the
CC protein it encodes will be useful in designing drugs to treat diseases
CC associated with environmental DNA damage
XX
SQ Sequence 1408 BP; 378 A; 318 C; 392 G; 320 T; 0 U; 0 Other;
Query Match 100.0%; Score 15; DB 2; Length 1408;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTATGACAGATCTG 15
DB 605 CGTATGACAGATCTG 591
RESULT 8
AAQ64088/c
ID AAQ64088 standard; DNA; 1755 BP.
XX
AC AAQ64088;
XX
DT 13-FEB-1995 (first entry)
XX
DE Mouse gene participating in homologous recombination.
XX
KW Homologous recombination; Rad51; recA; gene therapy; ss.
XX
OS Mus musculus.
XX
PH Key Location/Qualifiers
FT CDS 176..1195
FT /*tag= a
XX
PN JP06141863-A.
XX
PD 24-MAY-1994.
XX
PF 10-NOV-1992; 92JP-00299714.
XX
PR 10-NOV-1992; 92JP-00299714.
XX
PS (MORI/) MORITA T.
PS (MATS/) MATSUSHIRO A.
XX
DR WPI; 1994-205025/25.
DR P-PSDB; AAR54070.
XX
PT Mouse gene participating in homologous recombination reaction - useful
PT for improving the frequency of homologous recombination in gene therapy.
XX
PS Claim 4; Page 5-6; 8pp; Japanese.
XX
CC A mouse gene participating in homologous recombination, partic.
CC homologous to S. cerevisiae Rad51 and E. coli recA, is given in AAQ64088.
CC The gene improves the frequency of homologous recombination useful in
CC gene therapy and in the prepn. of disease model animals
XX
SQ Sequence 1755 BP; 485 A; 367 C; 467 G; 436 T; 0 U; 0 Other;

```

Query Match      100.0%; Score 15; DB 2; Length 1755;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
DB 592 CGTATGACAGATCTG 578

RESULT 9
AAA37710/c
ID AAA37710 standard; mRNA; 2229 BP.
XX AAA37710;
AC
XX 22-NOV-2000 (first entry)
XX
XX Human Rad51 mRNA.
XX
XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS9; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_binding 1..15
FT /tag= a
FT /bound_moiety= "AS4"
FT misc_binding 158..177
FT /tag= b
FT /bound_moiety= "AS5"
FT CDS 233..1252
FT /tag= c
FT /product= "Rad51"
FT misc_binding 311..328
FT /tag= d
FT /bound_moiety= "AS3"
FT misc_binding 425..438
FT /tag= e
FT /bound_moiety= "AS1"
FT misc_binding 635..649
FT /tag= f
FT /bound_moiety= "AS2"
FT misc_binding 1524..1545
FT /tag= g
FT /bound_moiety= "AS6"
FT misc_binding 1881..1902
FT /tag= h
FT /bound_moiety= "AS7"
FT misc_binding 1911..1933
FT /tag= i
FT /bound_moiety= "AS8"
FT misc_binding 2038..2060
FT /tag= j
FT /bound_moiety= "AS9"
XX
XX WO200047231-A2.
XX
XX 17-AUG-2000.
XX
XX 03-FEB-2000; 2000WO-US002881.
XX
XX 10-FEB-1999; 99US-0119578P.
XX 06-DEC-1999; 99US-00454495.
XX
XX (PANG-) PANGENE CORP.
XX
XX Reddy G;
XX
XX WPI; 2000-506091/45.
XX
XX Inhibiting cell proliferation useful for cancer therapy, comprises
PT

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PT administering Rad51 inhibitor in vivo.
XX
XX Disclosure; Fig 9b-9a; 42pp; English.
XX
XX This sequence is the human Rad51 mRNA sequence. Antisense inhibitors of
CC this sequence can be used in a method for inhibiting cell proliferation.
CC They can also be used in methods for inducing sensitivity to radiation
CC and DNA damaging chemotherapeutics in an individual and in a method for
CC prolonging survival in an individual with cancer. The methods and
CC antisense molecules are useful for inhibiting cell proliferation,
CC especially cancerous cell proliferation, for inducing sensitivity to
CC radiation and DNA damaging chemotherapeutics in individuals and for
CC prolonging survival in an individual with cancer. Kits for carrying out
CC the methods may be used to diagnose and/or treat cancer and for
CC adjunctive therapy. Note: In the specification, the 3' end of this
CC sequence is shown in figure 9a, while the 5' end of this sequence is
CC given in figure 9b
XX
XX Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;
SQ
Query Match      100.0%; Score 15; DB 3; Length 2229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
DB 649 CGTATGACAGATCTG 635

RESULT 10
AAS01209/c
ID AAS01209 standard; cDNA; 2229 BP.
XX
XX AAS01209;
XX
XX 04-JUL-2001 (first entry)
XX
XX Human RAD51 cDNA sequence.
DE
XX
XX Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
KW arthritis; graft rejection; inflammatory bowel disease; surgery;
KW angioplasty; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH primer_bind complement(403..425)
FT /tag= a
FT /note= "Binds antisense oligonucleotide AS6"
FT primer_bind complement(761..782)
FT /tag= b
FT /note= "Binds antisense oligonucleotide AS7"
FT primer_bind complement(791..813)
FT /tag= c
FT /note= "Binds antisense oligonucleotide AS8"
FT primer_bind complement(918..940)
FT /tag= d
FT /note= "Binds antisense oligonucleotide AS9"
FT primer_bind complement(1110..1115)
FT /tag= e
FT /note= "Binds antisense oligonucleotide AS4"
FT primer_bind complement(1258..1267)
FT /tag= f
FT /note= "Binds antisense oligonucleotide AS5"
FT primer_bind complement(1413..1424)
FT /tag= g
FT /note= "Binds antisense oligonucleotide AS3"
FT primer_bind complement(1455..1468)
FT /tag= h
FT /note= "Binds antisense oligonucleotide AS1"
FT primer_bind complement(1745..1759)
FT /tag= i
FT /note= "Binds antisense oligonucleotide AS2"
FT

```

```

XX PN WC200119397-A1.
XX PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-US025838.
XX PR 17-SEP-1999; 99US-0154616P.
XX PR 06-DEC-1999; 99US-00455300.
XX PA (PANG-) PANGENE CORP.
XX PI Reddy G;
XX DR WPI; 2001-244704/25.
XX PT Inhibiting cell proliferation for treating arthritis, graft rejection,
XX PT inflammatory bowel disease, cancer, proliferation induced after medical
XX PT procedure, involves administering Rad51 antibody or its fragment to cell.
XX PS Disclosure; Fig 15; 102pp; English.
XX CC The sequence represents the coding sequence of human Rad51. Rad51 protein
XX CC is defective in repair of damaged DNA, genetic recombination and the
XX CC recombinational repair of DNA lesions, and plays a central role in
XX CC cancer. The sequence was used to design antisense oligonucleotides which
XX CC were used to study down-regulation of Rad51 protein in human brain,
XX CC breast and prostate cells. Inhibiting cell proliferation involves
XX CC administering to a cell a Rad51 antibody or its fragment. The Rad51
XX CC antibody or its fragment is useful for inhibiting cell proliferation, for
XX CC treating disease states such as cancer, autoimmune disease, arthritis,
XX CC graft rejection, inflammatory bowel disease, proliferation induced after
XX CC medical procedures such as surgery, angioplasty etc. in humans and
XX CC animals
XX SQ Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;
Query Match 93.3%; Score 14; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTATGACAGATCTG 15
DB 1758 CGTATGACAGATCTG 1744
RESULT 11
ABZ23355/c
ID ABZ23355 standard; cDNA; 470 BP.
AC ABZ23355;
AC ABZ23355;
DT 07-APR-2003 (first entry)
DE Nucleotide sequence of a fragment of porcine RAD51 cDNA.
XX Antigenic determinant; immunotolerance; cell therapy; liver condition;
XX xenotransplantation; heart condition; pancreatic condition;
XX kidney condition; lung condition; RAD51; ss.
XX Sus sp.
XX WC200292791-A1.
XX 21-NOV-2002.
XX 14-MAY-2002; 2002WO-US015307.
XX 14-MAY-2001; 2001US-0291394P.
XX 13-AUG-2001; 2001US-0312125P.
XX 21-MAR-2002; 2002US-0367090P.
XX (STEL-) STELL.
XX PA

XX PI Liljedahl M, Marcantonio D, Aspland SE;
XX DR WPI; 2003-120679/11.
XX PF Novel genetically engineered cell in which a gene comprising an antigenic
XX PT determinant recognized by a recipient organism has been disrupted, useful
XX PT in cell therapy or xenotransplantation.
XX XX Example 9; Page 44-45; 97pp; English.
XX CC The specification describes genetically engineered cell in which at least
XX CC one gene encoding a polypeptide comprising an antigenic determinant which
XX CC is recognized by a desired recipient organism or at least one gene which
XX CC encodes a protein associated with the synthesis of a molecule comprising
XX CC the antigenic determinant has been disrupted. The genetically engineered
XX CC cell has a reduced level of immunogenicity in the recipient and can be
XX CC safely transplanted across species. It reduces the amount of medication
XX CC required to induce a state of immunotolerance in the host. The genetically
XX CC engineered cells of the invention are useful in cell therapy, or to
XX CC produce tissues or organs for use in xenotransplantation. They are useful
XX CC for treating heart conditions (e.g., valvular heart disease), liver
XX CC conditions (e.g., liver cirrhosis), pancreatic conditions (e.g.,
XX CC diabetes), kidney conditions (e.g., primary glomerulonephritis), lung
XX CC conditions (e.g., cystic fibrosis), Alzheimer's disease, stroke,
XX CC Parkinson's disease, cataracts and Creutzfeldt-Jacob disease. The present
XX CC sequence represents a PCR-amplified fragment of porcine RAD51 cDNA. The
XX CC fragment is used as a probe to identify homologous sequence to enhance
XX CC homologous recombination in the course of the invention
XX SQ Sequence 470 BP; 135 A; 112 C; 117 G; 106 T; 0 U; 0 Other;
Query Match 93.3%; Score 14; DB 7; Length 470;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTATGACAGATCTG 15
DB 224 GTATGACAGATCTG 211
RESULT 12
AAH28846/c
ID AAH28846 standard; DNA; 510 BP.
XX AC AAH28846;
XX 17-JUL-2001 (first entry)
XX DE Drosophila melanogaster essential gene fragment, SEQ ID NO: 35.
XX DE Drosophila melanogaster; fruit fly; essential gene; screening assay;
XX KW pesticide; crop protection; chromosome 3; ds.
XX OS Drosophila melanogaster.
XX PN WO200118547-A1.
XX 15-MAR-2001.
XX 06-SEP-2000; 2000WO-GB003444.
XX 07-SEP-1999; 99GB-00021009.
XX (UNITU) UNIV GLASGOW.
XX Davies RW, Kaiser K, Yang MY;
XX WPI; 2001-281436/29.
XX Screening assays for used for identifying compounds having a
XX PT physiological effect on proteins identified as being essential.
XX

```

PS Claim 1; Page 136; 695pp; English.
 XX
 CC The present sequence is part of an essential gene from *Drosophila*
 CC melanogaster. Lack of expression of the protein encoded by this gene
 CC leads to a lethal or semi-lethal phenotype. The invention relates to 902
 CC nucleic acid sequences from genes encoding proteins which are thought to
 CC be essential, and to a screening assay for identifying compounds which
 CC have a physiological effect on these proteins. Suitable compounds are
 CC useful as pesticides and may be used in conjunction with other pesticides
 CC and herbicides for crop protection. The gene corresponding to the present
 CC sequence is located on chromosome 3
 XX
 SQ Sequence 510 BP; 155 A; 111 C; 108 G; 136 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 4; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTATGACAGATCTG 15
 DB 316 GTATGACAGATCTG 303
 RESULT 13
 AAH29139
 ID AAH29139 standard; DNA; 513 BP.
 XX
 AC AAH29139;
 XX
 DT 17-JUL-2001 (first entry)
 XX
 DE *Drosophila melanogaster* essential gene fragment, SEQ ID NO: 328.
 XX
 KW *Drosophila melanogaster*; fruit fly; essential gene; screening assay;
 KW pesticide; crop protection; chromosome 3; ds.
 XX
 OS *Drosophila melanogaster*.
 XX
 PN WO200118547-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 06-SEP-2000; 2000WO-GB003444.
 XX
 PR 07-SEP-1999; 99GB-00021009.
 XX
 PA (UNIT) UNIV GLASGOW.
 XX
 PI Davies RW, Kaiser K, Yang MY;
 XX
 DR WPI; 2001-281436/29.
 XX
 FT Screening assays for used for identifying compounds having a
 FT physiological effect on proteins identified as being essential.
 XX
 PS Claim 1; Page 346; 695pp; English.
 XX
 CC The present sequence is part of an essential gene from *Drosophila*
 CC melanogaster. Lack of expression of the protein encoded by this gene
 CC leads to a lethal or semi-lethal phenotype. The invention relates to 902
 CC nucleic acid sequences from genes encoding proteins which are thought to
 CC be essential, and to a screening assay for identifying compounds which
 CC have a physiological effect on these proteins. Suitable compounds are
 CC useful as pesticides and may be used in conjunction with other pesticides
 CC and herbicides for crop protection. The gene corresponding to the present
 CC sequence is located on chromosome 3
 XX
 SQ Sequence 513 BP; 150 A; 94 C; 100 G; 169 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 4; Length 513;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTATGACAGATCTG 15
 DB 316 GTATGACAGATCTG 303
 RESULT 14
 AAF14202
 ID AAF14202 standard; cDNA; 649 BP.
 XX
 AC AAF14202;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE *Aspergillus cryzae* EST SEQ ID NO: 6725.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;
 KW *Aspergillus cryzae*; *Trichoderma reesei*; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis; ss.
 XX
 OS metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US007781.
 XX
 PR 22-MAR-1999; 99US-00273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
 XX
 DR WPI; 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 PT substrate of expressed sequence tags.
 XX
 PS Claim 88; Page 2744; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring the
 CC global expression of genes from FF cells allows the production potential
 CC of the microorganisms to be improved. New genes may be discovered.
 CC possible functions of unknown open reading frames can be identified and
 CC gene copy number variation and stability can be monitored. The expression
 CC of genes can be used to study how FF cells adapt to changes in culture
 CC conditions, environmental stress, spore morphogenesis, recombination,
 CC metabolic or catabolic pathway engineering. Using ESTs provides several
 CC advantages over genomic or random cDNA clones including elimination of
 CC redundancy as one spot on an array equals one gene or open reading frame,
 CC and organisation of the microarrays based on function of the genes.
 CC products to facilitate analysis of the results. AAF07478 to AAF1247
 CC represents ESTs from *Fusarium venenatum*; AAF11248 to AAF11853 represents
 CC ESTs from *Aspergillus niger*; AAF11854 to AAF14878 represents ESTs from
 CC *Aspergillus cryzae*; and AAF14879 to AAF15337 represents ESTs from
 CC *Trichoderma reesei*, which are all specifically claimed in the present
 CC invention
 XX
 SQ Sequence 649 BP; 151 A; 166 C; 168 G; 164 T; 0 U; 0 Other;
 Query Match 93.3%; Score 14; DB 3; Length 649;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCT 14
| | | | | | | | | | | | | |
Db 401 CGTATGACAGATCT 414

Qy 1 CGTATGACAGATCT 14
| | | | | | | | | | | | | |
Db 651 CGTATGACAGATCT 664

Search completed: March 21, 2004, 21:10:40
Job time : 287 secs

RESULT 15

ABK72962
ID ABK72962 standard; DNA; 1017 BP.

XX
AC ABK72962;

DT 13-AUG-2002 (first entry)

DE Bacillus licheniformis genomic sequence tag (GST) #253.

XX Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.

XX Bacillus licheniformis.

OS

XX WO200229113-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031437.

XX 06-OCT-2000; 2000US-00680598.

XX 27-MAR-2001; 2001US-0279526P.

XX (NOVO) NOVOZYMES BIOTECH INC.

PA (NOVO) NOVOZYMES AS.

XX Berka R, Clausen IG;

PI WPI; 2002-416684/44.

DR

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XX

Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag array.

Claim 4; SEQ ID NO 253; 200pp; English.

The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in one or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, environmental stress or other physiological provocation. Extensive follow-up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1017 BP; 296 A; 221 C; 296 G; 204 T; 0 U; 0 Other;

Query Match 93.3%; Score 14; DB 6; Length 1017;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 19:46:36 ; Search time 1531.5 Seconds
(without alignments)
424.516 Million cell updates/sec

Title: US-09-260-624A-2

Perfect score: 15

Sequence: 1 cgtatcacagatctg 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

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23: em.pat.*

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28: em.un.*

29: em.vi.*

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35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sv.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15	100.0	15	6	BD271100	Novel ant
2	15	100.0	15	6	AR343099	Sequence
3	15	100.0	15	6	AX099905	Sequence
4	15	100.0	15	6	AX099908	Sequence
5	15	100.0	15	6	AX492790	Sequence
6	15	100.0	357	6	E07534	Sequence
7	15	100.0	425	9	AY425955	Sequence
8	15	100.0	798	9	AF233739S4	Sequence
9	15	100.0	1160	9	H551RAD3	Sequence
10	15	100.0	1408	6	E09402	Sequence
11	15	100.0	1408	10	MUSRAD51A	Sequence
12	15	100.0	1645	6	AX771463	Sequence
13	15	100.0	1645	9	HUMRAD51B	Sequence
14	15	100.0	1682	6	E09404	Sequence
15	15	100.0	1745	10	MUSRAD51	Sequence
16	15	100.0	1755	6	E07535	Sequence
17	15	100.0	2121	10	BC027384	Sequence
18	15	100.0	2229	6	BD271098	Sequence
19	15	100.0	2229	6	AR343097	Sequence
20	15	100.0	2229	6	AX099913	Sequence
21	15	100.0	2229	9	HUMRAD51	Sequence
22	15	100.0	39521	9	AY196785	Sequence
23	15	100.0	58572	2	AC090935	Sequence
24	15	100.0	96678	2	HS477J10A	Sequence
25	15	100.0	156608	2	AF002445	Sequence
26	15	100.0	178248	9	AC012476	Sequence
27	15	100.0	182430	2	AC118799	Sequence
28	15	100.0	189540	10	AL772264	Sequence
29	15	100.0	190512	2	AC140278	Sequence
30	15	100.0	218553	2	AC079940	Sequence
31	15	100.0	221086	9	AC090359	Sequence
32	15	100.0	223408	2	AF001566	Sequence
33	15	100.0	262126	2	AC098502	Sequence
34	14	93.3	280	8	HVD234491	Sequence
35	14	93.3	510	6	AX093911	Sequence
36	14	93.3	513	6	AX094204	Sequence
37	14	93.3	576	8	CNS0198P	Sequence
38	14	93.3	745	3	BT011037	Sequence
39	14	93.3	920	14	BHV4GF80	Sequence
40	14	93.3	1017	6	AX431838	Sequence
41	14	93.3	1020	10	CORAD51	Sequence
42	14	93.3	1154	1	MSGAG	Sequence
43	14	93.3	1182	1	MSGAG	Sequence
44	14	93.3	1236	1	MAALANT	Sequence
45	14	93.3	1460	14	BHV4GENO	Sequence

ALIGNMENTS

RESULT 1	BD271100	15 bp	DNA	linear	PAT 07-AUG-2003
LOCUS	Novel antisense inhibition of Rad51.				
DEFINITION	Novel antisense inhibition of Rad51.				
ACCESSION	BD271100				
VERSION	BD271100.1	GI:33080868			
KEYWORDS	JP 2002536420-A/3.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 15)				
AUTHORS	Zeng, H., Reddy, G., Vallerga, A. and Zarling, D.A.				
TITLE	Novel antisense inhibition of Rad51				
JOURNAL	Patent: JP 2002536420-A 3 29-OCT-2002;				
	PANGENE CORP				

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COMMENT      OS      Artificial Sequence
PN          JP 2002536420-A/3
PD          29-OCT-2002
PF          03-FEB-2000 JP 2000598182
PI          10-FEB-1999 US 60/119578.06-DEC-1999 US 09/454495 PI
PR          HONG ZENG, GURUCHARAN REDDY, ANNE VALLERGA, DAVID A ZARLING PC
A61K45/00, A61K31/7088, A61K48/00, A61P1/00, A61P19/02, A61P29/00, PC
A61P35/00
PC          A61P37/06, G01N33/50
CC          Description of Artificial Sequence: synthetic FH      Key
FT          Location/Qualifiers
FT          source
FT          1. .15
FT          Location/Qualifiers
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FT          /mol_type="genomic DNA"
FT          /db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 2
AR343099
LOCUS      AR343099      15 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION      Sequence 3 from patent US 6576759.
ACCESSION      AR343099
VERSION      AR343099.1 GI:33738510
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Zeng, H., Reddy, G., Vallerga, A. and Zarling, D.A.
TITLE      Antisense inhibition of RAD51
JOURNAL      Patent: US 6576759-A 3 10-JUN-2003;
FEATURES
source
1. .15
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 3
AX099905
LOCUS      AX099905      15 bp      DNA      linear      PAT 02-APR-2001
DEFINITION      Sequence 8 from Patent WO0119397.
ACCESSION      AX099905
VERSION      AX099905.1 GI:13538931
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Reddy, G.
TITLE      Methods and compositions utilizing rad51
JOURNAL      Patent: WO 0119397-A 8 22-MAR-2001;
Pangene Corporation (US)

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FEATURES      Location/Qualifiers
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      1 CGTATGACAGATCTG 15

RESULT 4
AX099908/c
LOCUS      AX099908      15 bp      DNA      linear      PAT 02-APR-2001
DEFINITION      Sequence 11 from Patent WO0119397.
ACCESSION      AX099908
VERSION      AX099908.1 GI:13538934
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Reddy, G.
TITLE      Methods and compositions utilizing rad51
JOURNAL      Patent: WO 0119397-A 11 22-MAR-2001;
Pangene Corporation (US)
FEATURES
source
1. .15
/organism="synthetic construct"
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/note="Antisense oligonucleotide"

ORIGIN
Query Match      100.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTATGACAGATCTG 15
Db      15 CGTATGACAGATCTG 1

RESULT 5
AX492790
LOCUS      AX492790      15 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 2 from Patent WO02058738.
ACCESSION      AX492790
VERSION      AX492790.1 GI:23338473
KEYWORDS
SOURCE      synthetic construct
ORGANISM      synthetic construct
REFERENCE      1
AUTHORS      Zarling, D.A. and Reddy, G.
TITLE      Use of rad51 inhibitors for p53 gene therapy
JOURNAL      Patent: WO 02058738-A 2 01-AUG-2002;
PANGENE CORP (US)
FEATURES
source
1. .15
/organism="synthetic construct"
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/note="Antisense oligonucleotide"

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Query Match      100.0%; Score 15; DB 6; Length 15;

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Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 1 CGTATGACAGATCTG 15

RESULT 6
E07534/c
LOCUS E07534 357 bp RNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide including all of the base sequences possible to
            coding the important amino acid sequences in Rad 51.
ACCESSION E07534
VERSION E07534.1 GI:2175669
KEYWORDS JP 1994141863-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE Morita,T. and Matsushiro,A.
AUTHORS MURINE GENE PARTICIPATING IN HOMOLOGOUS RECOMBINING REACTION
TITLE Patent: JP 1994141863-A 3 24-MAY-1994;
JOURNAL MORITA TAKASHI, MATSUSHIRO AIZO
COMMENT OS None
        OC Artificial sequences.
        PN JP 1994141863-A/3
        PD 24-MAY-1994
        PF 10-NOV-1992 JP 1992299714
        PI MORITA TAKASHI, MATSUSHIRO AIZO
        PC C12N15/12,C12N1/19//C12Q1/68;
        CC strandedness: Single;
        CC topology: Linear;
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Best Local Similarity 100.0%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 36 CGTATGACAGATCTG 22

RESULT 7
AY425955/c
LOCUS AY425955 425 bp mRNA linear PRI 03-NOV-2003
DEFINITION Homo sapiens Rad51 mRNA, partial cds, alternatively spliced.
ACCESSION AY425955
VERSION AY425955.1 GI:38017104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        1 (bases 1 to 425)
REFERENCE Venables,J.P.
AUTHORS Alternative splicing in the testes
TITLE Unpublished
JOURNAL 2 (bases 1 to 425)
REFERENCE Venables,J.P.
AUTHORS Direct Submission
TITLE Submitted (01-OCT-2003) Institute of Human Genetics, Newcastle
JOURNAL University, International Centre for Life, Central Parkway,

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Newcastle upon Tyne, England NE1 3BZ, UK
Location/Qualifiers
1. .425
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<1. .197
/notes='alternatively spliced; similar to product encoded
by GenBank Accession Number D14134'
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/product='Rad51'
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RLSGSDSRASASRVVGTG'

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
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Db 384 CGTATGACAGATCTG 370

RESULT 8
AF233739S4/c
LOCUS AF233739S4 798 bp DNA linear PRI 21-SEP-2000
DEFINITION Homo sapiens RAD51 gene, exon 5.
ACCESSION AF233742
VERSION AF233742.1 GI:7767550
KEYWORDS
SEGMENT 4 of 7
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        1 (bases 1 to 798)
REFERENCE Ebbers,S.M. and Struwing,J.P.
AUTHORS Direct Submission
TITLE Submitted (09-FEB-2000) Laboratory of Population Genetics, National
JOURNAL Cancer Institute, 41 Library Dr., Room D702, Bethesda, MD
        20892-5060, USA

FEATURES
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/organism='Homo sapiens'
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/db_xref='taxon:9606'
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exon /number=5

ORIGIN
Query Match 100.0%; Score 15; DB 9; Length 798;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTATGACAGATCTG 15
    |||||
Db 497 CGTATGACAGATCTG 483

RESULT 9
HSS1RAD3/c
LOCUS HSS1RAD3 1160 bp DNA linear PRI 25-JAN-2002
DEFINITION Homo sapiens Rad51 gene, exon 5.
ACCESSION AFL65090
VERSION AFL65090.1 GI:5733652
KEYWORDS
SEGMENT 3 of 7

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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1160)
 AUTHORS Schmutte, C., Tomblin, G., Rhien, K., Sadoff, M.M., Schmutzler, R., von
 Deimling, A., and Fishel, R.
 TITLE Characterization of the human Rad51 genomic locus and examination
 of tumors with 15q14-15 loss of heterozygosity (LOH)
 JOURNAL Cancer Res. 59 (18), 4564-4569 (1999)
 MEDLINE 99421251
 PUBMED 10493508
 REFERENCE 2 (bases 1 to 1160)
 AUTHORS Schmutte, C., Tomblin, G., and Fishel, R.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUL-1999) Kimmel Cancer Center, Thomas Jefferson
 University, 233 S. 10th St., BLSB933, Philadelphia, PA 19107, USA
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 1. .1160
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
 Db 868 CGTATGACAGATCTG 854
 RESULT 10
 E09402/C
 LOCUS RAD51 structural gene. 1408 bp RNA linear PAT 29-SEP-1997
 DEFINITION E09402
 ACCESSION E09402.1 GI:22026029
 VERSION JP 1995143890-A/1.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1408)
 AUTHORS Shinohara, A., Numa, J., N., Ogawa, H. and Ogawa, T.
 TITLE RAD51 STRUCTURE GENE
 JOURNAL Patent: JP 1995143890-A 1 06-JUN-1995;
 TOYOBO CO LTD
 COMMENT OS Mus musculus (mouse)
 PN JP 1995143890-A/1
 PD 06-JUN-1995
 PF 28-MAY-1993 JP 1993127594
 PI SHINOHARA AKIRA, NUMA JITO NORIKO, OGAWA HIDEYUKI, OGAWA TOMOKO
 PC C12N15/12, C12N1/19, C12N5/10, C12P21/02, (C12N1/19, C12R1:865), PC
 (C12P21/02,
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 strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC feature is identified by experimental;
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 FT mat_peptide 190..1205
 /product="RAD51 protein"
 FT misc_feature 1. .1408
 /note="A structural gene recombining DNA and

repairing DNA
 damage.
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 /organism="Mus musculus"
 /mol_type="genomic RNA"
 /db_xref="taxon:10090"
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTATGACAGATCTG 15
 Db 605 CGTATGACAGATCTG 591
 RESULT 11
 MUSRAD51A/C
 LOCUS Mouse mRNA for RecA-like protein MmRad51, complete cds. 1408 bp mRNA linear ROD 29-MAY-2002
 DEFINITION Mouse mRNA for RecA-like protein MmRad51, complete cds.
 ACCESSION D13803
 VERSION D13803.1 GI:303702
 KEYWORDS ATPase; DNA repair; MmRad51; RecA-like protein; meiosis;
 recombination.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1408)
 AUTHORS Shinohara, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K. and Ogawa, T.
 TITLE Cloning of human, mouse and fission yeast recombination genes
 homologous to RAD51 and recA
 JOURNAL Nat. Genet. 4 (3), 239-243 (1993)
 MEDLINE 93364417
 PUBMED 8358431
 REFERENCE 2 (bases 1 to 1408)
 AUTHORS Shinohara, A.
 TITLE Direct Submission
 JOURNAL Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka
 University, Department of Biology, Toyonaka, Osaka 560, Japan
 (E-mail: c62528@center.osaka-u.ac.jp, Tel: 06-844-1151 (ex.4305),
 Fax: 06-841-2449)
 COMMENT Submitted (02-DEC-1992) to DDBJ by:
 Akira Shinohara
 Department of Biology
 Faculty of Science
 Osaka University
 1-1 Machikaneyama
 Toyonaka, Osaka 560
 Japan
 Phone: 06-844-1151 x4305
 Email: c62528@center.osaka-u.ac.jp
 Fax: 06-841-2449.
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 /db_xref="taxon:10090"
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 /note="map position 2F region."
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 189..1208
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LIVDSATLYRTDYSGRGELSARQMLRFLMLRLADEFGVAVITNQVAVQVDGA
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GDAND"

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 1408;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
Db 605 CGTATGACAGATCTG 591

FEATURES

source

RESULT 12
AX771463/c
LOCUS AX771463 1645 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 176 from Patent WO03004646.
ACCESSION AX771463
VERSION AX771463.1 GI:32438339
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1

REFERENCE O'Mahony, D.J., Byrne, D., Brayden, D., Lambkin, I. and Higgins, L.
AUTHORS Genetic analysis of Peyer's patches and M cells and methods and
TITLE compositions targeting Peyer's patches and M cell receptors
JOURNAL Patent: WO 03004646-A 176 16-JAN-2003;
ELAN CORPORATION, PIC (IE)

FEATURES

source

1..1645
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Query Match 100.0%; Score 15; DB 6; Length 1645;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15
Db 628 CGTATGACAGATCTG 614

RESULT 13

HUMRAD51B/c
LOCUS HUMRAD51B 1645 bp mRNA linear PRI 29-MAY-2002
DEFINITION Human mRNA for RecA-like protein HsRad51, complete cds.
ACCESSION D13804
VERSION D13804.1 GI:397826
KEYWORDS ATPase; DNA repair; HsRad51; RecA-like protein; meiosis; recombination.

SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1645)
AUTHORS Shinohara, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K. and Ogawa, T.
TITLE Cloning of human, mouse and fission yeast recombination genes homologous to RAD51 and recA

JOURNAL Nat. Genet. 4 (3), 239-243 (1993)
MEDLINE 93364417
PUBMED 8358431

REFERENCE

2 (bases 1 to 1645)

AUTHORS Shinohara, A.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka

University, Department of Biology; Toyonaka, Osaka 560, Japan
(E-mail: c62528@center.osaka-u.ac.jp, Tel: 06-844-1151 (ex. 4305),
Fax: 06-841-2449)

COMMENT On Sep 8, 1993 this sequence version replaced gi:303619.
Submitted (02-DEC-1992) to DDBJ by:

Akira Shinohara

Department of Biology

Faculty of Science

Osaka University

1-1 Machikaneyama

Toyonaka, Osaka 560

Japan

Phone: 06-844-1151 x4305

Email: c62528@center.osaka-u.ac.jp

Fax: 06-841-2449.

Location/Qualifiers

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gene

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DTGTFPRERLLAVAEYGLSGSDVLDNVAYAFNTHQTLQYQASAMVSRVAL
LIVDSATLYRTDYSGRGELSARQMLRFLMLRLADEFGVAVITNQVAVQVDGA
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1645

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Query Match 100.0%; Score 15; DB 9; Length 1645;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTATGACAGATCTG 15

Db 628 CGTATGACAGATCTG 614

RESULT 14

E09404/c
LOCUS E09404 1682 bp RNA linear PAT 29-SEP-1997
DEFINITION RAD51 structural gene.

ACCESSION E09404

VERSION E09404.1 GI:22026031

KEYWORDS JP 1995143890-A/3.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1682)

AUTHORS Shinohara, A., Namajio, N., Ogawa, H. and Ogawa, T.

TITLE RAD51 STRUCTURE GENE

JOURNAL Patent: JP 1995143890-A 3 06-JUN-1995;

TOYOBO CO LTD

OS Homo sapiens (human)

PN JP 1995143890-A/3

PD 06-JUN-1995

PF 28-MAY-1993 JP 1993127594

PI SHINOHARA AKIRA, NAMAJIO NORIKO, OGAWA HIDEYUKI, OGAWA TOMOKO

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PC      C12N15/12,C12N1/19,C12N5/10,C12P21/02,(C12N1/19,C12R1:865),PC
PC      (C12P21/02,
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CC      hypothetical: No;
CC      anti-sense: No;
CC      Feature is identified by experimental;
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FT      note='A structural gene coding a protein FT
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FT      DNA and repairs DNA damage'.
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGTATGACAGATCTG 15
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DB      631 CGTATGACAGATCTG 617
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RESULT 15
MUSRAD51/c
LOCUS      Mus musculus mRNA for Rad51 protein, complete cds.
DEFINITION      Mus musculus mRNA for Rad51 protein, complete cds.
ACCESSION      D13473
VERSION      D13473.1 GI:407348
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Morita,T., Yoshimura,Y., Yamamoto,A., Murata,K., Mori,M.,
Yamamoto,H. and Matsushiro,A.
A mouse homolog of the Escherichia coli recA and Saccharomyces
cerevisiae RAD51 genes
Proc. Natl. Acad. Sci. U.S.A. 90 (14), 6577-6580 (1993)
JOURNAL      93342035
MEDLINE      8341671
PUBMED
REFERENCE      2 (bases 1 to 1745)
AUTHORS      Morita,T.
TITLE      Direct Submission
JOURNAL      Submitted (26-OCT-1992) Takashi Morita, Research Institute for
Microbial Diseases, Dept. of Microbial Genetics, Osaka Univ.; 3-1
Yamadaoka, Suita, Osaka 565, Japan (Tel.81-6-6877-5121(ex.3172),
Fax:81-6-6876-2678)
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LIVDSATALYRTDYSGRGELSAQMHLARFLMLRLADEFGVAVVITNQVVAQVDGA
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polyA_site      1745
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Query Match      100.0%; Score 15; DB 10; Length 1745;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGTATGACAGATCTG 15
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DB      592 CGTATGACAGATCTG 578
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Search completed: March 21, 2004, 22:01:56
Job time : 1534.5 secs

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3	14	93.3	9542	3	US-08-968-685A-9		Sequence 9, Appli
4	13.4	89.3	1020	4	US-09-246-963A-6		Sequence 6, Appli
5	13.4	89.3	1029	4	US-09-328-352-1457		Sequence 1457, Ap
6	13.4	89.3	1181	3	US-09-329-796-2		Sequence 2, Appli
7	13.4	89.3	1479	4	US-09-328-352-2749		Sequence 2749, Ap
8	13.4	89.3	1574	4	US-09-246-963A-5		Sequence 5, Appli
9	13.4	89.3	2139	4	US-09-833-381-1020		Sequence 1020, Ap
10	13.4	89.3	2639	3	US-09-374-135-1		Sequence 1, Appli
11	13.4	89.3	2669	4	US-09-976-594-679		Sequence 679, App
12	13.4	89.3	2882	4	US-09-620-312D-531		Sequence 531, App
13	13.4	89.3	3621	4	US-08-956-171E-358		Sequence 358, App
14	13.4	89.3	5868	3	US-08-516-859A-3		Sequence 3, Appli
15	13.4	89.3	5868	4	US-09-586-472-3		Sequence 3, Appli
16	13.4	89.3	5868	4	US-09-528-706-3		Sequence 3, Appli
17	13.4	89.3	6171	1	US-08-459-568-1		Sequence 1, Appli
18	13.4	89.3	6171	2	US-08-399-411-1		Sequence 1, Appli
19	13.4	89.3	6171	3	US-08-516-859A-1		Sequence 1, Appli
20	13.4	89.3	6171	4	US-09-586-472-1		Sequence 1, Appli
21	13.4	89.3	6171	4	US-09-528-706-1		Sequence 1, Appli
22	13.4	89.3	8981	4	US-09-526-193A-20		Sequence 20, Appli
23	13	86.7	35	4	US-09-684-385-27		Sequence 27, Appli
24	13	86.7	35	4	US-09-684-385-41		Sequence 41, Appli
25	13	86.7	387	4	US-08-956-171E-2967		Sequence 2967, Ap
26	13	86.7	2060	1	US-08-480-547A-11		Sequence 11, Appli
27	13	86.7	2060	1	US-08-250-847B-11		Sequence 11, Appli

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2229
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-454-495-1

Query Match      100.0%; Score 15; DB 4; Length 2229;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGCTTCACCTAATTC 15
      |||||
Db      1548 GGCTTCACCTAATTC 1534

RESULT 3
US-08-968-685A-9/c
; Sequence 9, Application US/08968685A
; Patent No. 6214981
; GENERAL INFORMATION:
; APPLICANT: TUCKER, KENNETH
; APPLICANT: PLOSILA, LAURA
; TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,685A
; FILING DATE: No. 6214981ember 12, 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine F.
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 7969-060
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-968-685A-9

Query Match      93.3%; Score 14; DB 3; Length 9542;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGCTTCACCTAATTC 15
      |||||
Db      438 GGCTTCACCTAATTC 425

RESULT 4
US-09-246-963A-6/c
; Sequence 6, Application US/09246963A
; Patent No. 6541684
; GENERAL INFORMATION:

```

```

; APPLICANT: Bowen, Benjamin A.
; APPLICANT: Chamberlin, Mark A.
; APPLICANT: Drummond, Bruce J.
; APPLICANT: McElver, John A.
; APPLICANT: Rothstein, Rodney J.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Maize
; TITLE OF INVENTION: RAD51
; FILE REFERENCE: 033229/0750
; CURRENT APPLICATION NUMBER: US/09/246,963A
; CURRENT FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,745
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
US-09-246-963A-6

Query Match      89.3%; Score 13.4; DB 4; Length 1020;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGCTTCACCTAATTC 15
      |||||
Db      210 GGCTTCACCTAATTC 196

RESULT 5
US-09-328-352-1457/c
; Sequence 1457, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1457
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1457

Query Match      89.3%; Score 13.4; DB 4; Length 1029;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGCTTCACCTAATTC 15
      |||||
Db      96 GGCTTCACCTAATTC 82

RESULT 6
US-09-329-796-2
; Sequence 2, Application US/09329796
; Patent No. 6291174
; GENERAL INFORMATION:
; APPLICANT: Ning Li
; APPLICANT: Changxin WU
; APPLICANT: Yaofeng ZHAO
; TITLE OF INVENTION: DNA MARKERS FOR PIG LITTER SIZE
; FILE REFERENCE: 064727.0104
; CURRENT APPLICATION NUMBER: US/09/329,796
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/088,963
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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LENGTH: 1181
TYPE: DNA
ORGANISM: Sus scrofa
US-09-329-796-2

Query Match 89.3%; Score 13.4; DB 3; Length 1181;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 1165 GGCTTCACTAATTC 1179

RESULT 7

US-09-328-352-2749
Sequence 2749, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 2749

LENGTH: 1479

TYPE: DNA

ORGANISM: Acinetobacter baumannii

US-09-328-352-2749

Query Match 89.3%; Score 13.4; DB 4; Length 1479;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 1317 GGCTTCACTAATTC 1331

RESULT 8

US-09-246-963A-5/c

Sequence 5, Application US/09246963A

Patent No. 6541684

GENERAL INFORMATION:

APPLICANT: Bowen, Benjamin A.

APPLICANT: Chamberlin, Mark A.

APPLICANT: Drummond, Bruce J.

APPLICANT: McElver, John A.

APPLICANT: Rothstein, Rodney J.

TITLE OF INVENTION: Nucleotide Sequences Encoding Maize

FILE OF INVENTION: PAD51

FILE REFERENCE: 033229/0750

CURRENT APPLICATION NUMBER: US/09/246,963A

CURRENT FILING DATE: 1999-02-09

PRIOR APPLICATION NUMBER: US 60/074,745

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 1574

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: CDS

LOCATION: (73)....(1092)

US-09-246-963A-5

Query Match 89.3%; Score 13.4; DB 4; Length 1574;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 282 GGCTTCACTAATTC 268

RESULT 9

US-09-833-381-1020/c

Sequence 1020, Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1020

LENGTH: 2139

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)....(2139)

OTHER INFORMATION: n = A,T,C or G

US-09-833-381-1020

Query Match 89.3%; Score 13.4; DB 4; Length 2139;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 1608 GGCTTCACTAATTC 1594

RESULT 10

US-09-374-135-1/c

Sequence 1, Application US/09374135

Patent No. 6277972

GENERAL INFORMATION:

APPLICANT: Afar, Daniel E.

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahan

APPLICANT: Raitano, Arthur B.

APPLICANT: Saffran, Douglas C.

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND

FILE OF INVENTION: SECRETED BY PROSTATE AND BLADDER CANCER CELLS

FILE REFERENCE: 1703-017.US1

CURRENT APPLICATION NUMBER: US/09/374,135

CURRENT FILING DATE: 1999-08-10

PRIOR APPLICATION NUMBER: 60/095,982

PRIOR FILING DATE: 1998-08-10

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 2639

TYPE: DNA

ORGANISM: Homo sapiens

US-09-374-135-1

Query Match 89.3%; Score 13.4; DB 3; Length 2639;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15
DB 766 GGCTTCACTAATTC 752

RESULT 11
US-09-976-594-679
; Sequence 679, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 679
; LENGTH: 2669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1325741.20
; NAME/KEY: unsure
; LOCATION: 196, 205-224
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-679
Query Match 89.3%; Score 13.4; DB 4; Length 2669;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 71 GGCTTCTCAATTC 85
RESULT 12
US-09-620-312D-531/c
; Sequence 531, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP22
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 531
; LENGTH: 2682
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)...(2286)
US-09-620-312D-531
Query Match 89.3%; Score 13.4; DB 4; Length 2682;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 522 GGCTTCACTAATTC 508
RESULT 13
US-08-956-171E-358
; Sequence 358, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 358:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3621 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 358:
US-08-956-171E-358
Query Match 89.3%; Score 13.4; DB 4; Length 3621;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 1133 GGCTTCACTAATTC 1147

RESULT 14
US-08-516-859A-3/c
Sequence 3, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 121..5278
US-08-516-859A-3
Query Match 89.3%; Score 13.4; DB 3; Length 5868;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 5333 GGCTTCACTGATTC 5319

RESULT 15
US-09-586-472-3/c
Sequence 3, Application US/09586472
Patent No. 6323335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5868 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 121..5278
US-09-586-472-3
Query Match 89.3%; Score 13.4; DB 4; Length 5868;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
Db 5333 GGCTTCACTGATTC 5319
Search completed: March 21, 2004, 23:24:30
Job time : 61.5 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 18:17:32 ; Search time 282 Seconds
(without alignments)
225.968 Million cell updates/sec

Title: US-09-260-624A-1
Perfect score: 15
Sequence: 1 gggttcactaatcc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	3	AAA37712 Human Rad
2	15	100.0	15	4	AA01203 Human RAD
3	15	100.0	15	4	AA01194 Human RAD
4	15	100.0	15	6	AA013240 Antisense
5	15	100.0	20	4	AAf59439 Human Rad
6	15	100.0	1024	2	AB283420 Toxicolog
7	15	100.0	1408	2	Aa911761 Mouse Rad
8	15	100.0	1682	2	Aa911763 Human Gen
9	15	100.0	1755	2	Aa911763 Human Gen
10	15	100.0	2229	3	AA011209 Human RAD
11	15	100.0	2229	4	AA011209 Human RAD
12	15	100.0	21565	8	ADA02555 Mouse Ly6
13	15	100.0	21565	9	AD72293 Mouse Ly6
14	15	100.0	349980	5	Aa411223 Pyrococcus
15	14	93.3	18	7	AB23353 Forward P
16	14	93.3	379	4	Aa189144 Human pol
17	14	93.3	392	7	AB262850 Arabidops
18	14	93.3	470	7	AB23355 Nucleotid
19	14	93.3	498	3	AA069207 Bacteriop
20	14	93.3	582	5	AB233558 Human pro
21	14	93.3	1641	3	AA038441 Arabidops
22	14	93.3	2000	6	AB15287 Arabidops
23	14	93.3	2086	7	ADA53015 Human cod

C	24	14	93.3	9542	5	AA004029
C	25	14	93.3	9542	7	ABX93525
C	26	14	93.3	56506	3	AA069168 Bacteriop
C	27	13.4	89.3	60	6	ABN40306 Human spt
C	28	13.4	89.3	101	6	ABK76843 Bacillus
C	29	13.4	89.3	132	2	AAQ76733 Human gen
C	30	13.4	89.3	157	3	AAQ76733 Human sec
C	31	13.4	89.3	300	7	AB240806 N. gonorr
C	32	13.4	89.3	305	2	ABV88366 EST clone
C	33	13.4	89.3	351	5	ABV51730 Human pro
C	34	13.4	89.3	367	4	ABA46368 Human bre
C	35	13.4	89.3	367	4	ABA26546 Probe H50
C	36	13.4	89.3	367	4	AAK30559 Human bon
C	37	13.4	89.3	367	4	AB330224 Human liv
C	38	13.4	89.3	367	6	AB305218 Human ORF
C	39	13.4	89.3	387	6	ABN78458 Human ORF
C	40	13.4	89.3	411	2	AAV88121 EST clone
C	41	13.4	89.3	416	3	AA09763 Human sec
C	42	13.4	89.3	435	7	ACF03925 Rice endo
C	43	13.4	89.3	437	1	AAH90934 Y22 heavy
C	44	13.4	89.3	465	5	AAH81642 Human dif
C	45	13.4	89.3	470	3	AA076558 Human ORF

ALIGNMENTS

RESULT 1
AAA37712
ID AAA37712 standard; DNA; 15 BP.
XX
AC AAA37712;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human Rad51 antisense inhibitor AS1.
XX
KW Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS1; ss.
XX
OS Homo sapiens.
XX
PN WO200047231-A2.
XX
PD 17-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US002881.
XX
PR 10-FEB-1999; 99US-0119578P.
PR 06-DEC-1999; 99US-00454495.
XX
XX (PANG-) PANGENE CORP.
Reddy G;
WPI; 2000-506091/45.
Inhibiting cell proliferation useful for cancer therapy, comprises administering Rad51 inhibitor in vivo.
Example 1; Page 25; 42pp; English.
This sequence represents an antisense inhibitor of human Rad51, designated AS1 (also referred to as R51AS1). The antisense inhibitors can be used in a method of the invention, for inhibiting cell proliferation. They can also be used in methods for inducing sensitivity to radiation and DNA damaging chemotherapeutics in an individual and in a method for prolonging survival in an individual with cancer. The methods and antisense molecules are useful for inhibiting cell proliferation, especially cancerous cell proliferation, for inducing sensitivity to radiation and DNA damaging chemotherapeutics in individuals and for prolonging survival in an individual with cancer. Kits for carrying out the methods may be used to diagnose and/or treat cancer and for

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeiser K;
Alen P;

WPI; 2003-268322/26.

Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity.

Claim 1; Page 200; 455pp; English.

The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB282842 to AB284764, or their fragments of at least 20 nucleotides, or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals

Sequence 1024 BP; 267 A; 223 C; 311 G; 223 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 7; Length 1024;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACTAATTC 15
Db 418 GGCTTCACTAATTC 404

RESULT 7

AAQ91761/c
ID AAQ91761 standard; cDNA to mRNA; 1408 BP.

AC AAQ91761;

15-FEB-1996 (first entry)

Mouse Rad51 gene, encodes protein involved in DNA repair.

DNA mismatch repair; DNA recombination; site-specific; unwinding;
right-handed helical nucleoprotein; RAD51; mouse; recA; topoisomerase;
ss.

Mus musculus.

Key Location/Qualifiers
CDS 199..1208

/*tag= a
/product= "RAD51"

JP07143890-A.

06-JUN-1995.

28-MAY-1993; 93JP-00127594.

28-MAY-1993; 93JP-00127594.

(TOYM) TOYOBO KK.

WPI; 1995-236467/31.

P-PSDB; AAR78181.

Structural gene encoding RAD51, used in production of RAD51 - used to study drugs against diseases caused by DNA damage, e.g. by UV or X radiation, and to improve efficiency of gene therapy targeting.

Claim 1; Page 9-10; 19pp; Japanese.

The present sequence, isolated from mouse cDNA and localised to the F1 region of chromosome 2, is a specific example of DNA coding for a RAD51 protein having the amino acid sequence in AAR78181. The RAD51 protein, which contains an ATP-binding domain, is involved in DNA repair of mismatched base pairs and site-specific recombination in antibody gene rearrangements. The protein binds to double-stranded DNA to form a right-handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-form DNA. As a result, the helix is unwound. The Rad51 gene and the protein it encodes will be useful in designing drugs to treat diseases associated with environmental DNA damage

Sequence 1408 BP; 378 A; 318 C; 392 G; 320 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 1408;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACTAATTC 15
Db 395 GGCTTCACTAATTC 381

RESULT 8

AAQ91763/c

ID AAQ91763 standard; cDNA to mRNA; 1682 BP.

AC AAQ91763;

15-FEB-1996 (first entry)

Human Rad51 gene, encodes protein involved in DNA repair.

DNA mismatch repair; DNA recombination; site-specific; unwinding;
right-handed helical nucleoprotein; RAD51; human; recA; topoisomerase;
ss.

Homo sapiens.

Key Location/Qualifiers
CDS 215..1234

/*tag= a
/product= "RAD51"

JP07143890-A.

06-JUN-1995.

28-MAY-1993; 93JP-00127594.

28-MAY-1993; 93JP-00127594.

(TOYM) TOYOBO KK.

WPI; 1995-236467/31.

P-PSDB; AAR78183.

Structural gene encoding RAD51, used in production of RAD51 - used to study drugs against diseases caused by DNA damage, e.g. by UV or X

PT radiation, and to improve efficiency if gene therapy targetting.

XX Claim 1; Page 15-16; 19pp; Japanese.

XX The present sequence, isolated from human cDNA and localised to the q
CC region of chromosome 15, is a specific example of DNA coding for a RAD51
CC protein having the amino acid sequence in AAR78183. The RAD51 protein,
CC which contains an ATP-binding domain, is involved in DNA repair of
CC mismatched base pairs and site-specific recombination in antibody gene
CC rearrangements. The protein binds to double-stranded DNA to form a right-
CC handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-
CC form DNA. As a result, the helix is unwound. The Rad51 gene and the
CC protein it encodes will be useful in designing drugs to treat diseases
CC associated with environmental DNA damage

XX SQ Sequence 1682 BP; 477 A; 347 C; 456 G; 402 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 1682;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 421 GGCTTCACTAATTC 407

RESULT 9

AAQ64088/c

ID AAQ64088 standard; DNA; 1755 BP.

XX AC AAQ64088;

DT 13-FEB-1995 (first entry)

XX Mouse gene participating in homologous recombination.

DE Homologous recombination; Rad51; recA; gene therapy; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 176..1195

FT /*tag= a

XX JP06141863-A..

XX 24-MAY-1994.

XX 10-NOV-1992; 92JP-00299714.

XX 10-NOV-1992; 92JP-00299714.

XX (MORI/) MORITA T.

XX (MATS/) MATSUSHIRO A.

XX WPI; 1994-205025/25.

XX P-PSDB; AAR54070.

XX Mouse gene participating in homologous recombination reaction - useful
PT for improving the frequency of homologous recombination in gene therapy.

XX Claim 4; Page 5-6; 8pp; Japanese.

XX A mouse gene participating in homologous recombination, partic.
CC homologous to S. cerevisiae Rad51 and E. coli recA, is given in AAQ64088.
CC The gene improves the frequency of homologous recombination useful in
CC gene therapy and in the prepn. of disease model animals

XX SQ Sequence 1755 BP; 485 A; 367 C; 467 G; 436 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 1755;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 382 GGCTTCACTAATTC 368

RESULT 10

AAA37710/c

ID AAA37710 standard; mRNA; 2229 BP.

XX AC AAA37710;

XX DT 22-NOV-2000 (first entry)

XX Human Rad51 mRNA.

XX Antisense inhibitor; human; Rad51; cell proliferation; cancer survival;
KW radiation sensitivity; therapy; AS9; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_binding 1..15

FT /*tag= a

FT /bound_moiety= "AS4"

FT misc_binding 158..177

FT /*tag= b

FT /bound_moiety= "AS5"

FT CDS 233..1252

FT /*tag= c

FT /product= "Rad51"

FT misc_binding 311..328

FT /*tag= d

FT /bound_moiety= "AS3"

FT misc_binding 425..438

FT /*tag= e

FT /bound_moiety= "AS1"

FT misc_binding 635..649

FT /*tag= f

FT /bound_moiety= "AS2"

FT misc_binding 1524..1545

FT /*tag= g

FT /bound_moiety= "AS6"

FT misc_binding 1881..1902

FT /*tag= h

FT /bound_moiety= "AS7"

FT misc_binding 1911..1933

FT /*tag= i

FT /bound_moiety= "AS8"

FT misc_binding 2038..2060

FT /*tag= j

FT /bound_moiety= "AS9"

XX WO200047231-A2.

XX 17-AUG-2000.

XX 03-FEB-2000; 2000WO-US002881.

XX 10-FEB-1999; 99US-0119578P.

XX 06-DEC-1999; 99US-00454495.

XX (PANG-) PANGENE CORP.

XX Reddy G;

XX WPI; 2000-506091/45.

XX Inhibiting cell proliferation useful for cancer therapy, comprises
PT administering Rad51 inhibitor in vivo.
PS Disclosure; Fig 9b-9a; 42pp; English.
XX

CC This sequence is the human Rad51 mRNA sequence. Antisense inhibitors of
 CC this sequence can be used in a method for inhibiting cell proliferation.
 CC They can also be used in methods for inducing sensitivity to radiation
 CC and DNA damaging chemotherapeutics in an individual and in a method for
 CC prolonging survival in an individual with cancer. The methods and
 CC antisense molecules are useful for inhibiting cell proliferation,
 CC especially cancerous cell proliferation, for inducing sensitivity to
 CC radiation and DNA damaging chemotherapeutics in individuals and for
 CC prolonging survival in an individual with cancer. Kits for carrying out
 CC the methods may be used to diagnose and/or treat cancer and for
 CC adjunctive therapy. Note: In the specification, the 3' end of this
 CC sequence is shown in figure 9a, while the 5' end of this sequence is
 CC given in figure 9b
 XX
 SQ Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 3; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
 Db 439 GGCTTCACCTAATTC 425

RESULT 11
 AAS01209/C
 ID AAS01209 standard; cDNA; 2229 BP.

XX AAS01209;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human RAD51 cDNA sequence.
 XX
 KW Human; Rad51; antisense; drug screening; cancer; autoimmune disease;
 KW arthritis; graft rejection; inflammatory bowel disease; surgery;
 KW angioplasty; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key
 FT primer_bind Location/Qualifiers
 FT complement(403..425)
 FT /tag= a
 FT /note= "Binds antisense oligonucleotide AS6"
 FT primer_bind complement(761..782)
 FT /tag= b
 FT /note= "Binds antisense oligonucleotide AS7"
 FT primer_bind complement(791..813)
 FT /tag= c
 FT /note= "Binds antisense oligonucleotide AS8"
 FT primer_bind complement(918..940)
 FT /tag= d
 FT /note= "Binds antisense oligonucleotide AS9"
 FT primer_bind complement(1110..1115)
 FT /tag= e
 FT /note= "Binds antisense oligonucleotide AS4"
 FT primer_bind complement(1258..1267)
 FT /tag= f
 FT /note= "Binds antisense oligonucleotide AS5"
 FT primer_bind complement(1413..1424)
 FT /tag= g
 FT /note= "Binds antisense oligonucleotide AS3"
 FT primer_bind complement(1455..1468)
 FT /tag= h
 FT /note= "Binds antisense oligonucleotide AS1"
 FT primer_bind complement(1745..1759)
 FT /tag= i
 FT /note= "Binds antisense oligonucleotide AS2"
 XX
 PN WO200119397-A1.
 XX
 DT 22-MAR-2001.

XX 18-SEP-2000; 2000WO-US025838.
 XX
 XX 17-SEP-1999; 99US-0154616P.
 XX
 XX 06-DEC-1999; 99US-00455300.
 XX
 XX (PANG-) PANGENE CORP.
 XX
 XX Reddy G;
 XX
 XX WPI; 2001-244704/25.
 XX
 XX Inhibiting cell proliferation for treating arthritis, graft rejection,
 XX inflammatory bowel disease, cancer, proliferation induced after medical
 XX procedure, involves administering Rad51 antibody or its fragment to cell.
 XX
 XX Disclosure; Fig 15; 102pp; English.
 XX
 CC The sequence represents the coding sequence of human Rad51. Rad51 protein
 CC is defective in repair of damaged DNA, genetic recombination and the
 CC recombinational repair of DNA lesions, and plays a central role in
 CC cancer. The sequence was used to design antisense oligonucleotides which
 CC were used to study down-regulation of Rad51 protein in human brain,
 CC breast and prostate cells. Inhibiting cell proliferation involves
 CC administering to a cell a Rad51 antibody or its fragment. The Rad51
 CC antibody or its fragment is useful for inhibiting cell proliferation, for
 CC treating disease states such as cancer, autoimmune disease, arthritis,
 CC graft rejection, inflammatory bowel disease, proliferation induced after
 CC medical procedures such as surgery, angioplasty etc. in humans and
 CC animals
 XX
 SQ Sequence 2229 BP; 593 A; 472 C; 602 G; 562 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 4; Length 2229;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACCTAATTC 15
 Db 1548 GGCTTCACCTAATTC 1534

RESULT 12
 ADA02555/c
 ID ADA02555 standard; DNA; 21565 BP.

XX ADA02555;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX Mouse Ly6e carcinoma associated gene, SEQ ID NO:1073.
 XX
 KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
 KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
 KW Gene; ds.
 XX
 XX Mus sp.
 XX
 XX WO2003057146-A2.
 XX
 XX 17-JUL-2003.
 XX
 XX 26-DEC-2002; 2002WO-US041414.
 XX
 XX 26-DEC-2001; 2001US-00035832.
 XX
 XX (SAGR-) SAGRES DISCOVERY.
 XX
 XX Morris DW;
 XX
 XX WPI; 2003-587068/55.
 XX
 XX New recombinant nucleic acid encoding carcinoma associated protein,
 XX

PT useful for preparing compositions for treating carcinomas.

PS Claim 1; SEQ ID NO 1073; 245pp; English.

XX The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Query Match 21565 BP; 5397 A; 5271 C; 5466 G; 5371 T; 0 U; 60 Other;

XX Best Local Similarity 100.0%; Score 15; DB 8; Length 21565;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 8820 GGCTTCACTAATTC 8806

RESULT 13

ID ADB72293/c

ID ADB72293 standard; DNA; 21565 BP.

XX ADB72293;

XX 04-DEC-2003 (first entry)

XX Mouse Ly6e gene.

XX mouse; ds; cytostatic; Gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.

XX Mus sp.

XX WO2003008583-A2.

XX 30-JAN-2003.

XX 26-DEC-2001; 2001WO-US051291.

XX 02-MAR-2001; 2001US-0079586.

XX 23-OCT-2001; 2001US-00004113.

XX 08-NOV-2001; 2001US-00052482.

XX 30-NOV-2001; 2001US-00997722.

XX 20-DEC-2001; 2001US-00034650.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW, Engelhard EK;

XX WPI; 2003-239337/23.

XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.

XX Claim 1; SEQ ID NO 121; 2304pp; English.

XX The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.

XX Query Match 21565 BP; 5397 A; 5271 C; 5466 G; 5371 T; 0 U; 60 Other;

XX Best Local Similarity 100.0%; Score 15; DB 9; Length 21565;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 15

DB 8820 GGCTTCACTAATTC 8806

RESULT 14

AAH41223

ID AAH41223 standard; DNA; 349980 BP.

XX AAH41223;

XX 29-OCT-2001 (first entry)

XX Pyrococcus abyssi genomic fragment #2.

XX Hyperthermophilic archaeon; hyperthermophilic protein; ds.

XX Pyrococcus abyssi.

XX Key Location/Qualifiers

XX misc_feature 1..49980

XX /tag= a

XX /note= "This sequence overlaps with the 3' end of

XX AAF86431"

XX misc_feature 300001..349980

XX /tag= b

XX /note= "This sequence overlaps with the 5' end of

XX AAH41224"

XX PR2792651-A1.

XX 27-OCT-2000.

XX 21-APR-1999; 99FR-00005034.

XX 21-APR-1999; 99FR-00005034.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX (IFRE-) IFREMER INST FR RECH EXPL MER.

XX Forterre P, Thierry JC, Prieur D, Dietrich J, Lecompte O;

XX Querellou J, Weissenbach J, Saurin W, Heilig R;

XX WPI; 2001-126236/14.

XX New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry.

XX Claim 1; Page 265-361; 1657pp; French.

XX The present invention relates to the genomic sequence of Pyrococcus abyssi and P. abyssi proteins (see AAB96053-AAB96842). P. abyssi is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is a fragment of the genomic sequence of P. abyssi. The 5' end of this sequence overlaps with the 3' end of AAF86431 and the 3' end of this sequence overlaps with the 5' end of AAH41224. The

CC proteins of the present invention have various potential industrial uses,
CC since the proteins are stable at very high temperatures, some up to 110
CC degrees centigrade. Note: This patent is in the same patent family as
CC WO200065062, which contains additional sequences as shown in AAB99132-
CC AAB99143, AAH75903-AAH75920 and AAG66436
XX
SQ Sequence 349980 BP; 92953 A; 77841 C; 81831 G; 97355 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 349980;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 GGCTTCACTAATTC 15
DB 281481 GGCTTCACTAATTC 281495

RESULT 15
ABZ23353/c
ID ABZ23353 standard; DNA; 18 BP.

XX ABZ23353;

XX 07-APR-2003 (first entry)

Forward PCR primer used to amplify porcine RAD51 cDNA.

Antigenic determinant; immunotolerance; cell therapy; liver condition;
xenotransplantation; heart condition; pancreatic condition;
kidney condition; lung condition; RAD51; PCR; primer; ss.

XX Sus sp.

XX WO200292791-A1.

XX 21-NOV-2002.

XX 14-MAY-2002; 2002WO-US015307.

XX 14-MAY-2001; 2001US-0291394P.

XX 13-AUG-2001; 2001US-0312125P.

XX 21-MAR-2002; 2002US-0367090P.

XX (STEL-) STELL.

XX Liljedahl M, Marcantonio D, Aspland SE;

XX WPI; 2003-120679/11.
Novel genetically engineered cell in which a gene comprising an antigenic
determinant recognized by a recipient organism has been disrupted, useful
in cell therapy or xenotransplantation.

XX Example 9; Page 44; 97pp; English.

XX The specification describes genetically engineered cell in which at least
XX one gene encoding a polypeptide comprising an antigenic determinant which
XX is recognized by a desired recipient organism or at least one gene which
XX encodes a protein associated with the synthesis of a molecule comprising
XX the antigenic determinant has been disrupted. The genetically engineered
XX cell has a reduced level of immunogenicity in the recipient and can be
XX safely transplanted across species. It reduces the amount of medication
XX required to induce a state of immunotolerance in the host. The genetically
XX engineered cells of the invention are useful in cell therapy, or to
XX produce tissues or organs for use in xenotransplantation. They are useful
XX for treating heart conditions (e.g., valvular heart disease), liver
XX conditions (e.g., liver cirrhosis), pancreatic conditions (e.g.,
XX diabetes), kidney conditions (e.g., primary glomerulonephritis), lung
XX conditions (e.g., cystic fibrosis), Alzheimer's disease, stroke,
XX Parkinson's disease, cataracts and Creutzfeldt-Jacob disease. PCR primers
XX ABZ23353-54 were used to amplify a 407 bp fragment of porcine RAD51 cDNA.
XX The amplified fragment is used as a probe to identify homologous sequence
XX to enhance homologous recombination in the course of the invention

XX Sequence 18 BP; 8 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ Query Match 93.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTTCACTAATTC 14
DB 14 GGCTTCACTAATTC 1

Search completed: March 21, 2004, 21:10:35
Job time : 288 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 19:46:36 ; Search time 1531.5 Seconds
(without alignments)
424.516 Million cell updates/sec

Title: US-09-260-624a-1
Perfect score: 15
Sequence: 1 ggcttactaatcc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.ph.*
- 7: gb.pl.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.un.*
- 12: gb.vi.*
- 13: gb.vt.*
- 14: gb.vt.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pin.*
- 35: em.htg.rat.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.vt.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	15	100.0	15	6	BD271099	Novel ant
2	15	100.0	15	6	AR343098	Sequence
3	15	100.0	15	6	AX099904	Sequence
C 4	15	100.0	15	6	AX099907	Sequence
5	15	100.0	15	6	AX492789	Sequence
6	15	100.0	20	6	AX084202	Sequence
C 7	15	100.0	425	9	AY425955	Sequence
C 8	15	100.0	550	11	G80435	Sequence
C 9	15	100.0	1020	10	CGRAD51	Sequence
C 10	15	100.0	1389	8	AB080262	Sequence
C 11	15	100.0	1408	6	E09402	Sequence
C 12	15	100.0	1408	10	MUSRAD51A	Sequence
C 13	15	100.0	1417	9	BC001459	Sequence
C 14	15	100.0	1645	6	AX771463	Sequence
C 15	15	100.0	1645	9	HUMRAD51B	Sequence
C 16	15	100.0	1682	6	E09404	Sequence
C 17	15	100.0	1745	10	MUSRAD51	Sequence
C 18	15	100.0	1755	6	E07535	Sequence
C 19	15	100.0	2121	10	BC027384	Sequence
C 20	15	100.0	2229	6	BD271098	Sequence
C 21	15	100.0	2229	6	AR343097	Sequence
C 22	15	100.0	2229	6	AX099913	Sequence
C 23	15	100.0	2229	9	HUMRAD51	Sequence
C 24	15	100.0	2363	9	AF23373983	Sequence
C 25	15	100.0	3006	8	AB080361	Sequence
C 26	15	100.0	4823	10	CRUKCG1	Sequence
C 27	15	100.0	5799	10	MMU47737	Sequence
C 28	15	100.0	7606	9	HS51RAD1	Sequence
C 29	15	100.0	8153	9	AF203691	Sequence
C 30	15	100.0	21565	6	AX695446	Sequence
C 31	15	100.0	26083	3	U53339	Sequence
C 32	15	100.0	39521	9	AY196785	Sequence
C 33	15	100.0	59231	9	AL135937	Sequence
C 34	15	100.0	61332	2	AC084029	Sequence
C 35	15	100.0	61332	2	AC084029	Sequence
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C 37	15	100.0	147665	9	AL138691	Sequence
C 38	15	100.0	151186	2	AC068750	Sequence
C 39	15	100.0	153680	9	AC093003	Sequence
C 40	15	100.0	154494	2	AC120885	Sequence
C 41	15	100.0	154494	2	AC120885	Sequence
C 42	15	100.0	158510	9	AC079090	Sequence
C 43	15	100.0	166093	2	AC015462	Sequence
C 44	15	100.0	167857	9	AL138778	Sequence
C 45	15	100.0	169723	2	AC127987	Sequence

ALIGNMENTS

RESULT 1	BD271099	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
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DEFINITION	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003	
ACCESSION	BD271099	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
VERSION	BD271099.1	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
KEYWORDS	JP 2002536420-A/2.	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
SOURCE	synthetic construct	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
ORGANISM	artificial sequences.	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
REFERENCE	1 (bases 1 to 15)	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
AUTHORS	Zeng,H., Reddy,G., Valleria,A. and Zarling,D.A.	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
TITLE	Novel ant	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
JOURNAL	Patent: JP 2002536420-A 2 29-OCT-2002;	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003
	PANGENE CORP	Novel ant	15 bp	DNA	linear	PAT 07-AUG-2003

COMMENT OS Artificial Sequence
PN JP 2002536420-A/2
PD 29-OCT-2002
PF 03-FEB-2000 JP 2000598182
PR 10-FEB-1999 US 80/119578,06-DEC-1999 US 09/454495 PI
HONG ZENG, GURUCHARAN REDDY, ANNE VALLERGA, DAVID A ZARLING PC
A61K45/00, A61K31/7088, A61K48/00, A61P19/02, A61P29/00, PC
A61P35/00,
PC A61P37/06, G01N33/50
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCTTCACTAATTC 15
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AR343098
LOCUS AR343098 15 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6576759.
ACCESSION AR343098
VERSION AR343098.1 GI:33738509
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Zeng, H., Reddy, G., Vallerger, A. and Zarling, D.A.
TITLE Antisense inhibition of RAD51
JOURNAL Patent: US 6576759-A 2 10-JUN-2003;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GGCTTCACTAATTC 15
RESULT 3
AX099904
LOCUS AX099904 15 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 7 from Patent WO0119397.
ACCESSION AX099904
VERSION AX099904.1 GI:13538930
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Reddy, G.
TITLE Methods and compositions utilizing rad51
JOURNAL Patent: WO 0119397-A 7 22-MAR-2001;
Pangene Corporation (US)

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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGCTTCACTAATTC 15
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Db 1 GGCTTCACTAATTC 15
RESULT 4
AX099907/c
LOCUS AX099907 15 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 10 from Patent WO0119397.
ACCESSION AX099907
VERSION AX099907.1 GI:13538933
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Reddy, G.
TITLE Methods and compositions utilizing rad51
JOURNAL Patent: WO 0119397-A 10 22-MAR-2001;
Pangene Corporation (US)
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/note="Antisense oligonucleotide"
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15 GGCTTCACTAATTC 1
RESULT 5
AX492789
LOCUS AX492789 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO02058738.
ACCESSION AX492789
VERSION AX492789.1 GI:23338472
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Zarling, D.A. and Reddy, G.
TITLE Use of rad51 inhibitors for p53 gene therapy
JOURNAL Patent: WO 02058738-A 1 01-AUG-2002;
PANGENE CORP (US)
FEATURES
source
Location/Qualifiers
1.15
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/db_xref="taxon:32630"
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGCTTCACCTAATCC 15

RESULT 6
AX084202
LOCUS AX084202 20 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 18 from Patent WO0111369.
ACCESSION AX084202
VERSION AX084202.1 GI:13185709
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Sturzebecher, H.W. and Reddy, G.
TITLE Cancer treatments and diagnostics utilizing rad51 related molecules
and methods
JOURNAL Patent: WO 0111369-A 18 15-FEB-2001;
Pangene Corporation (US)
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Qy 1 GGCTTCACCTAATCC 15
Db 2 GGCTTCACCTAATCC 16

RESULT 7
AY425955/c
LOCUS AY425955 425 bp mRNA linear PRI 03-NOV-2003
DEFINITION Homo sapiens Rad51 mRNA, partial cds, alternatively spliced.
ACCESSION AY425955
VERSION AY425955.1 GI:38017104
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venables, J.P.
TITLE Alternative splicing in the testes
JOURNAL Unpublished
REFERENCE 2
AUTHORS Venables, J.P.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) Institute of Human Genetics, Newcastle
University, International Centre for Life, Central Parkway,
Newcastle upon Tyne, England NE1 3BZ, UK
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1..425
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/db_xref="taxon:9606"
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/product="Rad51"

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTTCACCTAATCC 15
Db 53 GGCTTCACCTAATCC 39

RESULT 8
G80435
LOCUS G80435 550 bp DNA linear STS 06-SEP-2002
DEFINITION S210P6047FH1.T0 BALB/cByJ Mus musculus STS genomic, sequence tagged
site.
ACCESSION G80435
VERSION G80435.1 GI:22731191
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Wade, C.
TITLE Polymorphism Structure in the Mouse
JOURNAL Unpublished (2002)
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 550
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.
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Best Local Similarity 100.0%; Pred. No. 5e+02;
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Db 465 GGCTTCACCTAATCC 451

RESULT 9
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RLSGSSDSRASASRVVGTIG"

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LOCUS CGRAD51 1020 bp mRNA linear ROD 05-JUN-1998
DEFINITION C-griseus mRNA for RAD51 protein.
ACCESSION Y08202
VERSION Y08202.1 GI:1552257
KEYWORDS DNA repair; RAD51 gene.
SOURCE Cricetulus griseus (Chinese hamster)
ORGANISM Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Cricetulus.
REFERENCE 1. Vispe,S., Cazaux,C., Lesca,C. and Defais,M.
Overexpression of Rad51 protein stimulates homologous recombination
and increases resistance of mammalian cells to ionizing radiation
Nucleic Acids Res. 26 (12), 2859-2864 (1998)
JOURNAL 98278998
MEDLINE 9611228
REFERENCE 2. (bases 1 to 1020)
AUTHORS Vispe,S.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-1996) S. Vispe, CNRS, IPBS, 205 route de
Narbonne, F- 31400 Toulouse, FRANCE
FEATURES Location/Qualifiers
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LIVDSATALRYTDYSGRGELSARQMLFLRLMLRLADBEFGVAVITNOVAQVDA
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Query Match 100.0%; Score 15; DB 10; Length 1020;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCTTCACCTAATTC 15
Db 207 GGCTTCACCTAATTC 193
RESULT 10
AB080262/c
LOCUS AB080262 1389 bp mRNA linear PLN 23-FEB-2002
DEFINITION Oryza sativa (japonica cultivar-group) OsRad51A1 mRNA for Rad51,
complete cds.
ACCESSION AB080262
VERSION AB080262.1 GI:18874070
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1. Shimizu,T., Mimida,N., Nakamura,S., Kawasaki,S., Nakashima,M.,

Osakabe,K., Toki,S. and Ichikawa,H.
Homologous recombination related genes, Rad51 in rice
Published Only in Database (2002)
REFERENCE 2. (bases 1 to 1389)
AUTHORS Shimizu,T., Mimida,N., Nakamura,S., Kawasaki,S., Nakashima,M.,
Osakabe,K., Toki,S. and Ichikawa,H.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Naozumi Mimida, National Institute of
Agrobiological Sciences, Department of Plant Biotechnology,
Kannonda2-1-2, Tsuba, Ibaraki 305-8602, Japan
Nannda2-1-2, Tsuba, Ibaraki 305-8602, Japan
IS-mail: mmdeaffrc.go.jp, Tel:81-298-38-7442, Fax:81-298-38-7073)
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DAEGTFPRYLLAVRGLSGADVLDNVAARGFTDHTQLLYQASAMVGSRYAL
LIVDSATALRYTDYSGRGELSARQMLFLRLMLRLADBEFGVAVITNOVAQVDS
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ADVKD"
ORIGIN
Query Match 100.0%; Score 15; DB 8; Length 1389;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCTTCACCTAATTC 15
Db 300 GGCTTCACCTAATTC 286
RESULT 11
E09402/c
LOCUS E09402 1408 bp RNA linear PAT 29-SEP-1997
DEFINITION RAD51 structural gene.
ACCESSION E09402
VERSION E09402.1 GI:22026029
KEYWORDS JP 1995143890-A/1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1. (bases 1 to 1408)
AUTHORS Shinohara,A., Namajio,N., Ogawa,H. and Ogawa,T.
TITLE RAD51 STRUCTURE GENE
JOURNAL Patent: JP 1995143890-A 1 06-JUN-1995;
COMMENT TOYOCO CO LTD
OS Mus musculus (mouse)
PN JP 1995143890-A/1
PD 06-JUN-1995
PF 28-MAY-1993 JP 1993127594
PI SHINOHARA AKIRA, NAMAJIO NORIKO, OGAWA HIDEYUKI, OGAWA TOMOKO
PC GI2N15/12, CI2N1/19, CI2N5/10, CI2P21/02, (CI2N1/19, CI2R1/865), PC
(CI2P21/02,
PC CI2R1/865), (CI2P21/02, CI2R1/19), (CI2P21/02, CI2R1/91); CC
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC feature is identified by experimental;
FH Location/Qualifiers

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  Db      395 GGCTTCACTAATTC 381
RESULT 12
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LOCUS      Mus musculus
DEFINITION      Mouse mRNA for RecA-like protein. MmRad51, complete cds.
ACCESSION      D13803
VERSION      D13803.1 GI:303702
KEYWORDS      ATPase; DNA repair; MmRad51; RecA-like protein; meiosis;
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 1408)
AUTHORS      Shinozaki, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K. and Ogawa, T.
TITLE      Cloning of human, mouse and fission yeast recombination genes
JOURNAL      Nat. Genet. 4 (3), 239-243 (1993)
MEDLINE      93364417
PUBMED      8358431
REFERENCE      2 (bases 1 to 1408)
AUTHORS      Shinozaki, A.
DIRECT SUBMISSION
  Submitted (02-DEC-1992) Akira Shinozaki, Faculty of Science, Osaka
  University, Department of Biology, Toyonaka, Osaka 560, Japan
  (E-mail: c62528@center.osaka-u.ac.jp, Tel: 06-844-1151 (ex. 4305),
  Fax: 06-841-2449)
  Submitted (02-DEC-1992) to DDBJ by:
  Akira Shinozaki
  Department of Biology
  Faculty of Science
  Osaka University
  1-1 Machikaneyama
  Toyonaka, Osaka 560
  Japan
  Phone: 06-844-1151 x4305
  Email: c62528@center.osaka-u.ac.jp
  Fax: 06-841-2449.
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DTGSKDLKLQGGIETGSIITMFEETGKTQICHTLAVTCQLPIGRGGEKAMVI
DTGTFRFRERLLAVERGLSGSDVLDNAVARGENTDHTQQLLYQASAMMVEGRYAL
LIVDSATALYRTDYSGRGELSGARQMLRFLRLMLRLADEFGVAVITNQVAQVDGA
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  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY      1 GGCTTCACTAATTC 15
  Db      395 GGCTTCACTAATTC 381
RESULT 13
BC001459/c
LOCUS      Homo sapiens
DEFINITION      Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae),
transcript variant 2, mRNA (cDNA clone MGC:2244 IMAGE:3139011),
complete cds.
ACCESSION      BC001459
VERSION      BC001459.2 GI:33876241
KEYWORDS      MGC.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 1417)
AUTHORS      Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, J., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buotow, K.H., Schaefer, C.F., Shat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heist, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, D.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalski, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL      MEDLINE
PUBMED      22388257
REFERENCE      2 (bases 1 to 1417)
AUTHORS      Strausberg, R.
DIRECT SUBMISSION
  Submitted (12-DEC-2000) National Institutes of Health, Mammalian
  Gene Collection (MGC), Cancer Genomics Office, National Cancer
  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
  USA
  NIH-MGC Project URL: http://mgc.nci.nih.gov
  On Aug 19, 2003 this sequence version replaced gi:13655202.
  Contact: MGC help desk
  Email: cgapbs-remail.nih.gov

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Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nigri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-J., Karlins, E., Kwong, P., Lalic, P., Legaspi, R.,
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Place: 4 Row: n Column: 19
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 19924132.

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QY 1 GGCTTCACCTAATCC 15
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RESULT 14

AX771463/c AX771463 1645 bp DNA linear PAT 02-JUL-2003
 LOCUS Sequence 176 from Patent WO03004646.
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 KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS O'Mahony, D.J., Byrne, D., Brayden, D., Lambkin, I. and Higgins, L.
 TITLE Genetic analysis of Peyer's patches and M cells and methods and
 compositions targeting Peyer's patches and M cell receptors
 JOURNAL Patent: WO 03004646-A 176 16-JAN-2003;
 ELAN CORPORATION, Plc (IE)

FEATURES

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RESULT 15

HUMRAD51B/c HUMRAD51B 1645 bp mRNA linear PRI 29-MAY-2002
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 DEFINITION
 ACCESSION D13804
 VERSION D13804.1 GI:397826
 KEYWORDS ATPase; DNA repair; HsRad51; RecA-like protein; meiosis;
 recombination.

SOURCE

ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shinozaki, A., Ogawa, H., Matsuda, Y., Ushio, N., Ikeo, K. and Ogawa, T.
 TITLE Cloning of human, mouse and fission yeast recombination genes
 homologous to RAD51 and recA
 JOURNAL Nat. Genet. 4 (3), 239-243 (1993)

MEDLINE

PUBMED 93364417
 8358431

REFERENCE

AUTHORS Direct Submission
 TITLE Submitted (02-DEC-1992) Akira Shinohara, Faculty of Science, Osaka
 University, Department of Biology, Toyonaka, Osaka 560, Japan
 (E-mail: c62528@center.osaka-u.ac.jp, Tel: 06-844-1151 (ex.4305),
 Fax: 06-841-2449)

COMMENT

On Sep 8, 1993 this sequence version replaced gi:303619.
 Submitted (02-DEC-1992) to DDBJ by:

Akira Shinohara
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 Faculty of Science
 Osaka University
 1-1 Machikaneyama
 Toyonaka, Osaka 560
 Japan

Phone: 06-844-1151 x4305
 Email: c62528@center.osaka-u.ac.jp
 Fax: 06-841-2449

FEATURES

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Best Local Similarity 100.0%; Fred. No. 5e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCCTCACTAATTC 15
Db 418 GGCCTCACTAATTC 404
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Search completed: March 21, 2004, 22:01:53
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